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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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genbank110 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_pr3 39:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi
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(1-1447) from US08878177.seq
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SUMMARIES

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| 11 12 13 | 10 8 9 | 4450 | Result No. |
| 353 341 337 | 353 358 358 | 344 446 382 | Score |
| 24.4 23.6 23.3 | 25.1 25.1 24.7 24.5 | 29.9 20.8 20.8 | Query Match |
| 133746 2954 588 | 2916 2938 1673 4403 | 1516 3166 3126 762 816 | Query Match Length |
| 26 26 | 26 | 22222 2006 2006 2006 | BG BG |
| AP000022 HUMERGBFLI S72865 | A36461 HSHUMFLI S45205 XLFLIG | GGERG HUMERG2 HUMERG11 S72621 S66169 MMFLI1 | ij |
| Homo sapiens genomic D Human ERGB transcripti EWSEWS-erg=EWS-er | Sequence 2 from Patent H.sapiens HUMFLI-1 mRN Fli-1=Friend leukemia X.laevis mRNA XLFLI. | G.gallus ERG mRNA. Human erg 2 gene encodi Human erg protein (ets EWSerg (transloca Erg-3=immunoglobulin h Mouse fil-1 mRNA for r | Description |
| 2.47e-293 5.68e-282 3.46e-278 | 0.00e+00 0.00e+00 4.52e-298 3.15e-295 | 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 | Pred. No. |

| RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL SOURCE OUTHORS TITLE SOURCE AUTHORS TITLE GENTURES SOURCE SOURCE CDS | C C C C C C C C C C C C C C C C C C C |
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| ALIGNMENTS 1 GGERG 1516 bp RNA VRT G.gallus ERG mRNA. X77159 g790439 ERG gene. Chicken. Gallus gallus Eukaryotae; mitochondrial eukaryotes; Metazoa; Cho Vertebrata; Archosauria; Aves; Meognathae; Gallifo Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 1516) Dhordain, P., Dewitte, F., Desbiens, X., Stehelin, D. Mesodermal expression of the chicken erg gene asso precartilaginous condensation and cartilage differ Mech. Dev. 50 (1), 17-28 (1995) 95329425 2 (bases 1 to 1516) Duterque-Coquillaud, M. Direct Submission Submisted (17-JAN-1994) M. Duterque-Coquillaud, CN Oncologie Moleculaire, Institut Pasteur, 1 rue Callile, FRANCE Location/Qualifiers 1.1516 Jorganisme "Gallus gallus" //thssue_typee "Boleen" //tlssue_typee "Boleen" /clone_lib="lambda gt10" 631499 /gene="ERG" /cdon_start=1 /cdon_start=1 /db_xref="PID:g790440" | 325 22.5 1932 26 HUMFLIIA COUTRIX MRNA, comp 320 22.1 3490 21 CCRNAFLI COUTRIX MRNA, 279 19.3 66352 28 HSY17293 Homo sapiens FIJ-1 gen 179 12.4 634 19 SULERG 15.2 10.4 1901 27 HSRNAFEY H.sapiens FIA for FEY 10.4 1901 28 HSRNAFEY H.sapiens FIA for FEY 10.4 1901 29 HMSETSI HAMBORI SETS HAMBORI |
| 27-APR-1995 rdata; rdata; rmes; and ciated with entiation entiation mette, 59019 | Mmp 7.63e-267 NNA 3.11e-262 NNA 3.11e-263 NNA 3.11e-263 NNA 3.11e-263 NNA 3.11e-263 NNA 3.11e-263 NNA 3.11e-263 NNA 3.11e-251 NNA 3.11e-261 NN |

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SKMSPKYQQDWLSQPPARVTIKMECNPNQVNGSRNSPDDCSYAKGGKWYSSDNVGM
NYGSYMEEKH LPPPNMTINERKYLYPADPTLMSTDHYRQMLEWAVKEYGLPDVOILTE
QNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRL
MHARNITGGATFIFPNTSYYPEATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSS
STYPKTEDQRPQLDFYQGLGPTSSRLANPGSGGIQLWGPLEELLSDSSNSCTTWGES
STYPKTEDGPRQLDFYQGLGPTSSRLANPGSGGIQLWGPLEELLSDSSNSCTTWGFT
NGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFH
G1AQALQPHPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSFFAAPND
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GERKSKPNNNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLY
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/Codon_start=1
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atttaccttatgagcaagcgaggagatcagcgtggacgagtcacagccatcccactc---
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This sequence comes from Fig. 2A.
Map location: t(21;22)(q22;q12).
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PVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSH"
86...762
                                                                                                                                                                                                    /product="EWS-erg fusion protein type 1e"
/db_xref="piD:g633774"
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/translation="PTSYPPQTGSYSQAPSQYSQQSSSYGQQNLPYEPPRRSAWTGHG
HPTPQSKAAQPSPSTYPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLS
DSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNIMTK
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/gene="EWS"
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                                                            GenBank staff at the National Library of Medicine created thi entry [NCBI gibbsq 138523] from the original journal article.
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Ets proteins: new factors that
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/organism="Mus sp."
/db_xref="taxon:10095"
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CAGAAGATGAACTTTGTGTCTCCCCACCCTCCCGCTCTCCCAGTCACATCTTCCAGTTT
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                                                                                          cagaagatgaactttgtagctccccatccccctgctttgcccgtaacctcatccagctt
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                                                                                                                                                                                                                                                                                                                                          AGCCGCGCCCTCCGCTACTACTACGACAAAACATCATGACCAAGGTGCACGGGAAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aactccaactgcatcacctgggagggcacaaatggggagttcaagatgacagaccctgat
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/codon_start=1
/codon_start=1
/db_xref="plD:436277"
/translation="DDFORTLPSYNADILLSHLHYLRETPLPHLTSDDVDKALONSPR
LMHARNTGGAAFIFPNTSVYPEATQRITTRPDLPYEPPRRSAWTGHSHLTPQSKAAQP
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GTNGEFKWTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFD
FHGIAQALQPHPPESSLYKYPSDLPYWGSYHAHPQKNNFVSPHPPALPVTSSSF"

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/note="immunoglobulin
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/note="immunoglobulin heavy-chain
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                                                                                           CAGCCAGTGAGAGTCAATGTCAAGCGGGAGTATGACC---AC-ATG--AATGGATCCAGG
                                                                                                                                                                                                                                                                                                        GAGTCTCCGGTGGACTGCAGTGTCAGCAAATGTAACAAGCTGGTGGGCGGAGGCGAAGCC
                                                                                                                                             gaatatgggcaaacatcaaagatgagcccgcgcgttccccagcaggactggttatcacag
                                                                                                                                                                                                                                   TCAGCATACGGAGCGGCAGCCCATCTCCCCCAAGGCAGATATGACTGCTTCGGGGAGTCCT 364
 aattcacctgatgactgcagcgtggcaaaaggagggaaaatggttagcagttcagacaat
                                                                      cccccggccagagttaccattaagatggagtgtaacccaaaccaggttaatgggtcaagg
                                                                                                                                                                                 GACTACGGGCAGCCCCACAAAATCAACCCCCTGCCACCGCAGCAGGAGTGG--ATCA-AC
                                                                                                                                                                                                                  tgtgcctacggatcg-c--cccaccttgcaaagacagaaatgacagcctcctcttccagt
                                                                                                                                                                                                                                                                                       Submitted (08-MAY-1991) K. Letwin, Samuel Lunenfeld Res Mount Sinai Hospital, Div of Mol and Developmental Biol University Avenue, Toronto Ontario M5G 1X5, CANADA 2 (bases 1 to 1729)

Ben-David,Y., Giddens,E.B., Letwin,K. and Bernstein,A. Erythroleukemia induction by Friend murine leukemia virinsertional activation of a new member of the ets gene: Fil-1, closely linked to c-ets-1 Genes Dev. 5 (6), 908-918 (1991)
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/codon_start-1
/codon_start-1
/codon_start-1
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/product-"retrovirus integration site"
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NSYMDEKNGPPPPNMTINERRVIVPADPTLWTQEHVRQWLEWAIKEYGLMEIDTSFFQ
NMDGKELCKMNKEDFLRATSAYNTEVLLSHLSYLRESSLLAYNTTSHTDQSSRLNVKE
DPSYDSVRRGAWNNNMNSGLNKSPLLGSGOTMGKNTEQREPQPDPYQILGPTSSRLANP
GSGQIQLWGFLLELLSDSANASGITWEGTNGEFKMTDPDSVARRWGERKSKPNMYDK
LSRALRYYYDKNIMTKYHGKRYAYKFDEHGIAQALQPHFTETSMYKYPSDISYMPSYH
LSRALRYYYDKNIMTKYHGKRYAYKFDEHGIAQALQPHFTETSMYKYPSDISYMPSYH
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/evidence-expe
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                                 GGAGCAGCATCACAATACTGGACCTCCCCCACTGCTGGGATCTATCCAAACCCCCAG
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NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS
PAtent: WO 9323549-A 2 25-NOV-1993;
CENTRE NAT RECH SCIENT (FR)
Other publication FD 7777
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FLI-1 gene homologue.
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Inst. Curie, 26 rue D'Ulm,
2 (bases 1 to 2938)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                              GTGAGGCAATGGCTGGAGTGGGCCATAAAGGAGTATAGCTTGATGGAGAGATCGACACATCC
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//db_xrefts plD:g32530"
//translations "mbcTIKEALSVYSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQ
PHKINPLPPQQEWINQPVRVVKREYDHMNGSRESPVDCSVSKCSKLVGGGESNPMNY
NSYMDEKNGPPPPNMTINERRVIVPADPTLWTGPHYQRUPATKSYLMEIDTSFFQ
NMOCKELCKUNKEDFLAFTTLVNTEVLLSHLSYLRESSLLAYNTSTTDQSSRLSYKE
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GSGQIQLWQFFLLELLSDSANASCITWECTNGEFKMTDPDEVARRWGERKSKPNMYTOK
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AHQQKNVFYPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNYPRHPNTHYPSHLGS
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                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H. 1 (bases 1 to 1673)
Prasad,D.D., Rao,V.N. and Reddy,E.S.
Structure and expression of human Fli-1 gene Cancer Res. 52 (20), 5833-5837 (1992)
            GenBank staff at the National Library of Medicine entry (NCBI gibbsq 115336) from the original journ This sequence comes from Fig. 1A.

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fli gene;
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X66979
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2 (bases 1 to 4403)
Meyer,D., Wolff,C.M., Stiegler,P.,
                                                                                                                                                                                                                   Submitted (22-JUN-1992) C. Moleculaire et Cellulaire
                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; P
Pipidae; Xenopodinae; Xenopus.
1, (bases 1 to 4403)
                                                                                                        during embryogenesis in a crest cell distribution
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Xenopus laevis
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/organism-"Xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="unfertilized eggs"
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cgtcttgcaaatccagggagtgggcagatacagctatggcagttcctactggagcttctg
                                                                           acagaagaccagc---gtcctcagttagatccttatcagattcttggaccgaccagcagc
                                                                                                                                                       caca-gccatc-ccactcagtcaaaagctacccaacc-atcatcttcaacagtgcccaaa
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Similarity 68.2%;
749; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region),
                                                                                                                                                                                                                                                                      Submitted (11-MAY-1998) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)
                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (1998) In (Dases 1 to 133746) Hizakawa, M., Yamaguchi, H. and Imai, K. Direct Submission
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Homo sapiens genomic DNA, chromos
region), segment 15/15, complete
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                                                                                    24.4%;
Similarity 83.7%;
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                                                                     Conservative
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                                                                                                                                                      /chromosome="21"
/map="21q22.2"
29023 c 28295
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1. .133746
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/db_xref="taxon:9606"
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. No. 2.47e-293;
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M98833
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Papas, T.S. and Seth, A.
The ERGB/FLI1 gene: Isolation and characterization of of the family of human ETS transcription factors
Cell Growth Differ. 3, 705-713 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding protein; transcription factor. Homo sapiens (library: lambda gt10) cDNA to Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
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                                      Cell_type="r-cell"
/tissue_lib="lambda gt10"
/tissue_lib="lambda gt10"
/map="Chromosome 11, awaiting qualifier approval"
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/product="ErgB transcription factor"
/product="PrD:g182189"
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NMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLRESSLLAVNTTSPLEWALKSVESQH
NSYMDEXNGPPPNMTINNNSGLNKSPPLGGAQTISKNTEORPOPDTYGILGPTSSRLAND
GSGQIQLWGFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDK
LSRALRYYYDKNIMTKYHGKKYAYKFDPHGIAQALQPHPTSSMYKYPSDISYMPSQH
LSRALRYYYDKNIMTKYHGKKYAYKFDPHGIAQALQPHPTSSMYKYPSDISYMPSQH
LSRALRYYYDKNIMTKYHGKKYAYKFDPHGIAQALQPHPTSSMYKYPSDISYMPSQH
LSRALRYYYDKNIMTKYHGKKYAYKFDPHGIAQALQPHPTSSMYKYPSDISYMPSQH
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                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="CEM"
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Eutheria; Primates; Catarrhini; Hominidae; H
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Best Local
GAGGTGGCCAGGCGCTGGGGCGAGCGGAAAAGCAAGCCCAACATGAATTACGACAAGCTG
                                                                                      AACGCCAGCTGTATCACCTGGGAGGGGACCCAACGGGGAGTTCAAAATGACGGACCCCGAT
                                                                                                                                                                           CCTGGAAGCGGCCAGATCCAGCTGTGGCAATTCCTCCTGGAGCTGCTCTCCGACAGCGCCC
                                                                                                                                                                                                                                                         CAACGGCCCCAGCCAGATCCGTATCAGATCCTGGGCCCGACCAGCAGCAGTCGCCTAGCCAAC
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                                                                aactccaactgcatcacctgggagggcacaaatggggagttcaagatgacagaccctgat
                                                                                                                                                  ccagggagtgggcagatacagctatggcagttcctactggagcttctgtcggacagctcc
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Hromas, R., May, W., Denny, C., Raskind, W., Moore, J., Maki, Beck, E. and Klemsz, M.J.
Human FLI-1 localizes to chromosome 11024 and has an abo; transcript in neuroepithelloma
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                                                                /cell_type="erythroleukemia"
/tissue_type="blood"
/tissue_lib="lambda gt11 HEL 2'
/map="11q23-25"
join(1. .401,576. .1932)
/gene="FLI-1"
                                                                                                                                                                                                                                                                                                                                                                         Biophys. Acta 1172 (1-2),
                                                                                                                                                                                                                    /organism="Homo sapiens"
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/cell_line="HEL"
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                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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ATACAGAGCAACGGCCCCAGCCAGATCCGTATCAGATCCTGGGCCCGACCAGCAGTCGCC 1161
                                                           ACATGAATTCTGGCCTCAACAAAGTCCTCCCCTTGGAGGGGCACAAACGATCAGTAAGA 1101
                                                                                          gaataacaacaaggccagatttaccttatgagcaagcgaggagatcagcgtggacgagtc
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Similarity 68.3%;
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join(174. .401,576. .1700)
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PSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQPDPYQLIGPTSSRLANG
SGQ1QLMQFLLELSDSANASCITWEGTNGEFKNTDPDEVARRWGORKSKENMYDKL
SRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSUHA
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HQKVNFVPPPHPSSMPVTSSSFFGAASQYWTSTGGIYPNPNVPRHPNTHVPSHLGSYY
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YDRHDSSMPYTSSSFFGAASQYWTSTGGIYPNDYPRHPNTHVPSHLGSYY"
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/note="alternate"
/codon_start-1
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fli gene;
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Y14773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mager, A.M., Grapin-Botton, A., Ladjali, K., Meyer, D., Wolff, C.M., Stiegler, P., Bonnin, M.A. and Remy, P.
The avian fil gene is specifically expressed during embryogenesis in a subset of neural crest cells giving rise to mesenchyme Int. J. Dev. Biol. 42 (4), 561-572 (1998)
                                                                                                                                                                                                                                                                                                                                        Recherche, Scientifique, U.1
Descartes, 67084 Strasbourg
Related sequence Y14774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stiegler, P.
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1. .3490
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BASE COUNT
ORIGIN
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Best Local Similarity 79.2%;
Matches 434; Conservative
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                                          AAACCCCA 1457
                                                                                   atccagctttttgctgcccctaatccatactggaattcaccaactggaggcatctaccc
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Pred. No. 4.03e-262;
0; Mismatches 114; Indels
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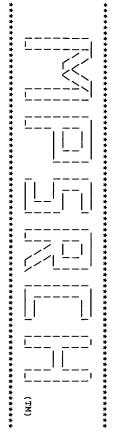
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Search completed: Sat Apr 10 10:21:10 1999 Job time : 3786 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

WPsrch_pp protein - protein database search, using Smith-Waterman algorithm Bun on:

Wed Apr 7 09:46:21 1999; MasPar time 27.16 Seconds 876.521 Million cell updates/sec

bular output not generated.

Title: >US-08-878-177-4
Description: (1-478) from US08878177.pep
Perfect Score: 3467

Sequence: 1 MASTIKEALSVVSEDQSLFE.....IYPNTRLPAAHMPSHLGTYY 478

Scoring table: PAM 150 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb16

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 48.382; Variance 88.436; scale 0.547

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| No. | Score | Match | Length DB | ₩ | ID | Description | Pred. No. |
|-----|-------|-------|-----------|----|--------|------------------------|-----------|
| 1 | 3126 | 90.2 | 478 1 | ω | Q90837 | ERG PROTEIN. | 0.00e+00 |
| 2 | 1401 | 40.4 | 385 | 4 | Q14319 | | 9.42e-281 |
| ω | 1267 | 36.5 | 254 | 4 | Q16199 | EWS-ERG FUSION PROTEIN | 5.03e-250 |
| 4 | 915 | 26.4 | 196 | 4 | Q16203 | EWS EWS-ERG=EWS-ER | 5.52e-170 |
| G | 592 | 17.1 | 188 | v | Q22355 | MID 1 | 4.81e-98 |
| σ | 555 | 16.0 | 208 | S | Q18579 | I. | 5.77e-90 |
| 7 | 543 | 15.7 | 238 | 4 | Q99581 | FEV PROTEIN. | 2.35e-87 |
| œ | 543 | 15.7 | 340 1 | F | 070132 | ETS DOMAIN TRANSCRIPTI | 2.35e-87 |
| 9 | 460 | 13.3 | 268 1 | ω | Q91744 | XE1-A DNA-BINDING PROT | 1.84e-69 |
| 10 | 454 | 13.1 | 336 | σ | 062804 | TRANSCRIPTION FACTOR G | 3.51e-68 |
| 11 | 449 | 13.0 | 559 | σ | Q26645 | ETS HOMOLOGUE. | 4.09e-67 |
| 12 | 444 | 12.8 | 426 | σ | 062803 | TRANSCRIPTION FACTOR E | 4.75e-66 |
| 13 | 406 | 11.7 | 393 | U | 061805 | C. ELEGANS LIN-1 (GB:U | 5.25e-58 |
| 14 | 406 | 11.7 | 441 | G | Q27378 | LIN-1. | 5.25e-58 |
| 15 | 404 | 11.7 | 494] | ū | 057586 | ETS-DOMAIN TRANSCRIPTI | 1.38e-57 |
| 16 | 391 | 11.3 | | 13 | 057566 | TRANSCRIPTION FACTOR G | 7.41e-55 |
| 17 | 373 | 10.8 | 64 | 4 | Q16031 | ERG-P55 (ALTERNATIVELY | 4.25e-51 |
| 18 | 336 | 9.7 | 76 | 4 | Q16198 | EWSFLI1 (FRAGMENT | 1.86e-43 |
| 19 | 326 | 9.4 | 663 | 4 | Q99607 | MYELOID ELF-1 LIKE FAC | 2.06e-41 |
| 20 | 323 | 9.3 | 521 | 4 | Q15725 | NERF-1A. | 8.42e-41 |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 |
|------------------------|------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|--|---------|------------------------|------------------------|------------------------|------------|--------------------|------------------------|------------------------|------------------------|------------------|------------------------|------------------------|----------|
| 213 | 226 | 224 | 225 | 225 | 225 | 227 | 227 | 228 | 241 | 243 | 265 | 265 | 265 | 270 | 269 | 279 | 288 | 296 | 298 | 303 | 316 | 321 | 323 | 323 |
| 6.1 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.6 | 7.0 | 7.0 | 7.6 | 7.6 | 7.6 | 7.8 | 7.8 | 8.0 | 8.3 | 8.5 | 8.6 | 8.7 | 9.1 | 9.3 | 9.3 | 9.3 |
| | | | | | ယ | | | | | | | 371 | | 507 | | | | 81 1 | | | | | 581 | S |
| σ | u | ഗ | 5 | ഗ | ഗ | G | IJ | u | σ | u | <u>; </u> | 4 | 4 | ъ | G | 'n | 4 | 14 | G | σ | υ | 4 | 4 | 4 |
| Q26070 | 044138 | Q25159 | Q25127 | Q25066 | Q23822 | Q26573 | Q25574 | Q16997 | 062767 | Q25573 | 035275 | P78545 | Q99718 | Q93320 | 001519 | 070273 | Q16324 | Q64998 | Q19695 | 001521 | 017057 | 060435 | Q15723 | Q15724 |
| ETS-1 PROTEIN (FRAGMEN | C50A2.4 PROTEIN. | ETS-1 PROTEIN (FRAGMEN | ETS-1 PROTEIN (FRAGMEN | ETS-1 PROTEIN (FRAGMEN | ETS PROTEIN (FRAGMENT) | ETS-1 PROTEIN (FRAGMEN | ETS-2 PROTEIN (FRAGMEN | ETS-2 PROTEIN (FRAGMEN | ERYTHROBLASTOSIS VIRUS | ETS-1 PROTEIN (FRAGMEN | ETS TRANSCRIPTION FACT | ESE-1B. | EPITHELIAL-SPECIFIC TR | HYPOTHETICAL PROTEIN C | SIMILARITY TO THE DNA- | EHF (EHF). | TLS ERG [TRANSLOCA | (TS1.1 MUTANT) V-ETS (| SIMILAR TO DNA BINDING | SIMILARITY TP THE DNA- | C24A1.2 PROTEIN. | ELF-1 RELATED PROTEIN. | ETS TRANSCRIPTION FACT | NERF-1B. |
| . 12e | 1.13e-21 | .70e | 1.75e-21 | .75e | 1.75e-21 | .32e | 7.32e-22 | . 74 | . 56 | 6.45e-25 | 41 | .41e | 3.41e-29 | 3.55e-30 | 5.58e-30 | 5.91e-32 | .58e- | 2.41e-35 | .56e- | .44e | 2.23e-39 | .15e- | 8.42e-41 | .42e- |

ALIGNMENTS

| Qy | В | Qy | 뭥 | VΩ | 뭥 | νQ | 망 | Ma Ma | SQ | DR : | א א | DR | ₹ 7 | RA | 2 2 | 8 R | R | 86 | 88 | S E | D C | 13.5 | RESULT |
|--|--|--|--|---|---|---|---|---|--|------------|------------------------------------|------------------------|-------------------------|--|--------------------|--------------------|---|--|----------------------|--------------|---|--------------|--|
| 181 PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEA 240 | 181 PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEA 240 | 121 NERRVIVPADPTIMSTDHVRQWIEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT 180 | 121 NERRVIYPADPTLMSTDHYRQWLEWAYKEYGLPDYDILLFQNIDGKELCKMTKDDFQRLT 180 | 61 PARVTIKMECNDNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 | 61 PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 | 1 MASTIKBALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDMLSQP 60 | 1 MASTIKEALSVYSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 | Query Match 90.2%; Score 3126; DB 13; Length 478; Best Local Similarity 92.1%; Pred. No. 0.00e+00; Matches 441; Conservative 10; Mismatches 26; Indels 2; Gaps 2; | SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; | 00178; Ets | PROSITE: PS00346: ETS_DOMAIN_1: 1. | EMBL; X77159; G790440; | MECH DEV 50:17-28(1995) | DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., | MEDLINE; 95329425. | SEQUENCE FROM N.A. | | EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES. | US GALLUS (CHICKEN). | ERG PROTEIN. | O1-JUN-1996 (TREMBERED: O1, LAST SEQUENCE UPDATE) | 01, CREATED) | LT 1 Q90837 PRELIMINARY; PRT; 478 AA. |

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Q14319;
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HROMAS R., MAY W.,
KLEMSZ M.J.;
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EMBL; M93255; G182661; -.
PROSITE: PS00345; ETS_DOMAIN_1: 1.
PROSITE; PS00346; ETS_DOMAIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
    436
                                        341
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                         SMPVTSSSFFGAASQYWTS-TGGIYPNPNVPRHPNTHVPSHLGSYY 385
                                                                                                                                                            NSG-LNKS-PPLG-GAQ----TISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFL
                                                                                                                                                                                                                                                                                                                                                    ESSL--LAYNTTSHT-DQSSRL-SVKE---D----P--S-Y-DSV-R---R-G-AWGNNM
                                                                                                                                                                                                                                                                                                                                                                                                           EHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNMTTNERRVIVPADATLVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPVTSSSFFAAPNPYWNSPTGGIYPNT---
                                                                                                       MTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYP-SDISYMPSYHAHQQKVNFVPPHPS
                                                                                                                                                                                                                                             RSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFL
                                                                                                                                                                                                                                                                                                                               ETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPYEQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNMTTNERRVIVPADPTLWST
                                                                                MTKVHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQPHAHPQKMNFVAPHPP
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G (TREMBLREL.
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llarity 56.4%;
Conservative
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 9.42e-281;
69; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RASKIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
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Best Local S
Matches 17
   Query Match
Best Local Similarity
Matches 129; Conser
                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 94314948.

GIOVANNIII M., BIEGEL J.A., SERRA M.

GIOVANNIEL B.S., EVANS G.A.;

CLIN. INVEST. 94:489-496(1994).

J. CLIN. INVEST. 94:489-496(1994).

EMBL; S72865; G633778; ...

PROSITE; PS00346; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996
01-NOV-1996
01-JUN-1998
EWS. . . EWS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q16203;
Q16203;
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Q16199;
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EUTHERIA; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-JUN-1998 (TREMBLREL. 06, EWS-ERG FUSION PROTEIN TYPE EWS-ERG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PFAM; PF00178; Ets. 1
NON_TER 1 1
SEQUENCE 254 AA; 28577 MW; 5
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                                                                                                                                   SEQUENCE
                                                                                                                                                                    PFAM; PF00178; NON_TER
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J. CLIN. INVEST 944.489-496(1994).
EMBL; S72621; G533774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 94314948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
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Local Similarity 77.7%;
ses 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPDLPYEQARRSAWTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPIENS (HUMAN)
RYOTA; METAZOA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKMNEVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYP-SDLPYMGSYHAHP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RALRYYYDKNIMTKVHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQPHAHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7-1996 (TREMBLREL. (7-1996 (TREMBLREL. (7-1998 (TREMBLREL. (7-1998 (TREMBLREL. (FWS-ERG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMATES
                                                                                                                                   196 AA;
   26.4%;
larity 73.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                 Ets.
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                                                                                                                                   22268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01, CREATED)
01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
FUSION PROTEIN TYPE 9E (FRA
                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1267;
Pred. No. 5.
20; Mismatc
Score 915; DB 4; L
Pred. No. 5.52e-170;
15; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
1E (FRAGMENT).
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                                                                                                                                   FBCD632E
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ches 28;
                                                                                                                                   CRC32;
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                                                                 Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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RP SEQUENCE ENCL.

RC STRAIN-BRISTOL N2;

RX MEDIJINE; 94150718.

RA MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,

RA BURTON J., CONNELL M., COPSEY J., COOPER J., COULSON A., CRAXTON M.,

RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,

RA HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,

RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTWING J., LLOYD C.,

RA MCMURRAY A., MORTINORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,

RA RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,

RONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,

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Best Local S
Matches 7
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               WATERSTON R.;
SUBMITIED (CCT-1995) TO EMBL/GENBANK/DDBJ DATA
EMBL; U39470; G1041871; -.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
COSMID T08H4.
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Q22355;
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STELLYES L.;
SUBMITTED (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA;
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                                                                                                                                                                                                                              DPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARR 349
                                                                                                                                                                                                                                                    DPYQILGPTSKNLAHSGSGQTQLWQFLLELLSDKRYSEVITWEGTQGEFKLVDPDEVARK 64
                                                                                                                                                                                                                                                                                                                                                                                               PF00178; Ets.
NCE 188 AA;
                                                                                                                                                                                                                                                                                                                Similarity
78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAZOA;
    (TREMBLREL.
                                                                PRELIMINARY;
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larity 77.2%;
Conservative
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601,
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                                                                                                                                                                                                                                                                                                              Score 592; DB 5; 1
Pred. No. 4.81e-98;
9; Mismatches 13
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LAST ANNOTATION UPDATE)
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                                                                208
                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
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                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                    Length 188
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Best Local S
Matches 6
Query Match
Best Local Similarity
Matches 70; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                Q99581;
Q99581;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD BURTON J., CONNELL M., COPEST J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMUTRAX A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH SONNHAMMER E., STADEN M., SHUSTOON J., THIERRY-MIEG J., THOMAS K., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                          MAGDELENAT H., DELATTRE O.;
ONCOGENE 14:1159-1164(1997).
ONCOGENE 14:1159-1164(1997).
EMBL; Y08976; E291921; -.
PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (APR-1996) TO EMBL/GENEMBL; U56966; G1293845; -.
PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PFAM; PF00178; Ets.
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                                                                                      SEQUENCE
                                                                                                                                                                                                                                         SEQUENCE FROM PETER, COUTUR!
                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                        FEV PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
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MEDLINE; 94150718.
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                                                                                                                                                                                                                   MAGDELENAT H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WATERSTON R.
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                                                                                                             PF00178;
                                                                                                                                                                                                                                       COUTURIER J.,
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                                                                                      238
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15.7%;
larity 73.7%;
Conservative
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                                                                                                                                                                                                                                       PACQUEMENT
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  Score
Pred.
13; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                         VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                      D4057DD0 CRC32;
re 543; DB 4;
1. No. 2.35e-87;
Mismatches 10
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                                                                                                                                                                                                                                       MICHON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
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                                          Length
    Indels
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Best Local S
Matches 7
                                                                Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O91744 PRELIMINARY; PRT; 268 AA. O91744; O1-NOV-1996 (TREMBLREL. 01, CREATED) O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UP 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION XEL-A DNA-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O70132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                    TISSUE-TOTAL OVARY FROM SINGLE FROG.
SALVATI F., MORABITO, MERENDINO, CARNEVALI;
SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA
EMBL, X65167; G517228;
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST SANOTATION UPDATE)
ETS DOMAIN TRANSCRIPTION FACTOR PET-1.
RATTUS NORVEGICUS (RAT).
RETTAZOA; CHORDATA; VERTEBRATA; TETRAPODA.
                                                                                                                                                                                                                                                                                                                                                                                                                          XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98127904.
FYODOROV D., NELSON T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE PHEOCHROMOCYTOMA; MEDLINE; 98127904.
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                   DNA-BINDING.
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BBL; U91679; G3033410; -.
OSITE; PS00345; ETS_DOMAIN_1; 1.
OSITE; PS00346; ETS_DOMAIN_2; 1.
QUENCE 340 AA; 35439 MW; B32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPNMNYDKLSRALRYYYDKNIMSKVHGKRYA-YRF
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Similarity 73.7%;
70; Conservation
                                                                h 13.3%;
Similarity 44.4%;
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RODENTIA.
                                                                                                                                                        268
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30805
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                                                                Score 460;
Pred. No. 1.
33; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 543; DB 11;
Pred. No. 2.35e-87;
13; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                  Mismatches 45;
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                                                                                     DB 13;
.84e-69;
                                                                                                                                                        CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                            TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UPDATE)
<del>--</del>
                                                                                                                                                                                                                                                                                                                BANKS
                                                                                                       Length 268,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            AMPHIBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMALIA;
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                                                                Gaps
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Best Local S
Matches 6
Query Match
Best Local Similarity
Matches 58; Conser
                                                                                                                                    RAO S.K., CHILDS G.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK
EMBL; L19541; G310662; -.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PRAM; PF00178; Ets.
SEQUENCE 559 AA; 62052 MW; 0F896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            062804 PRELIMINARY:
062804;
01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
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Q26645;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-1998
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR GABP ALPHA SUBUNIT (FRAGMENT).
OVIS ARIES (SHEEP).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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EZASHI T., EALY A.D., OSTROWSKI M.C., ROBERTS R.M.;

SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS

EMBL; AF057717; G3046690; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETS HOMOLOGUE.
STRONGYLOCENTROTUS
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                                                                                                                                                                                                                                                                                                                                                                                       FISSUE=EMBRYONIC;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUECHINOIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 46.7%; hes 63; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTAIKAIN-SSAKAAKVQ-RAPRISGEDRSSP-GNRTGN--NGQIQLWQFLLELLTDKDA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMYKYPSDLPYMSSY 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVYKFVCDLKTLIGY 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSN 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL.)
(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 AA; 38033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PURPURATUS (PURPLE SEA URCHIN); ECHINODERMATA; ECHINOZOA; ECH
                                13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %01,
10,01
                                                                                                                                                                                                                                                                                                               EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 454; DB 6;
Pred. No. 3.51e-68;
32; Mismatches 34
                                Score 449; DB 5;
Pred. No. 4.09e-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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   Mismatches
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                                                                                                                                       CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32;
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                                                                                                                                                                                                                                                                                                               DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECHINOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 336
                                                                   Length
   Indels
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   'n
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   Gaps
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        061805;
061805;
                                                                                                                                                                              WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTINING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SNITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O62803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
C. ELEGANS LIN-1 (GB.038937), PARTIAL CDS, CONTAINS
DOMAINS (PFAM: ETS.HMM, SCORE: 162.78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

EZASHI T., EALY A.D., OSTROWSKI M.C., ROBERTS R.M.;

SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AF057716; G3046688; -

EMBL; AF057716; G3046688; -

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVIS ARIES (SHEEP).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; ARTIODACTYLA.
       STRAIN-BRISTOL N2;
MILLER N., BIEWALD T
SUBMITTED (MAY-1998)
                                                                                                                                      THIERRY-MIEG J., THOMAS K WATSON A., WEINSTOCK L., NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TREMBLREL 07, 01-AUG-1998 (TREMBLREL 07, 01-AUG-1998 (TREMBLREL 07, TRANSCRIPTION FACTOR ETS-2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302
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hes 59; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEKLSRGLRYYYDKNIIHKT-SGKRYYYRFLCDLQNLLGF 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAN-PGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%;
59.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACOELOMATES; NEMATODA;
          EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                              K., VAUDIN M., VAU WILKINSON-SPROAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7, CREATED)
7, LAST SEQUENCE UPI
7, LAST ANNOTATION 1
2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 444; DB 6;
Pred. No. 4.75e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPDATE)
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                                                                                                                                                              WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SERAIN-BRISTOL N.2;
WATERSTON R.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DAY
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DAY
R EMBL; AF067606; G3158478;
R EMBL; AF067606; G3158478;
R PROSITE; PS00346; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.

TOTTENCE 393 AA; 42884 MW; C907FB61 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96127909.

BETTEL G.J., TUCK S., GREENWALD I.

GENES DEV. 9:3149-3162(1995).

EMBL; U38937; G1161370; -.

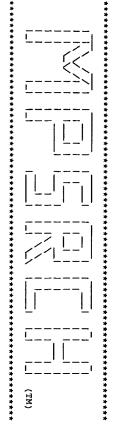
EMBL; U38936; G1161370; JOINED.

EMBL; U38935; G1161372; -.

EMBL; U38935; G1161372; -.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JLT 14
027378
027378;
01-NOV-1996
01-NOV-1996
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LIN-1.
                                                                                                                                                                                      057586
057586;
057586;
01-JUN-1998
01-JUN-1998
01-AUG-1998
                                                                                                                             PEA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL.
SEQUENCE
BRACHYDANIO RERIO (ZEBRAFISH)
EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIN-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLWQFLLELLQQDQNGDIIEWTRGTDGEFRLIDAEAVARKWGQRKAKPHNNYDKLSRAL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RYYYDKNIMTKVHPPESSMYKY
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48; Conservative
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Similarity 58.5%;
48; Conservative
                                                                                                                                                              3 (TREMBLREL. 06, CREATED)
3 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
3 (TREMBLREL. 07, LAST ANNOTATION UPDAT
TRANSCRIPTION FACTOR PEA3.
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(TREMBLREL.
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Pred. No. 5.25e-58;
17; Mismatches 15;
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LAST ANNOTATION
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Pred. No. 5.25e-58;
17; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144
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                                    CYPRINIFORMES
                                                              (ZEBRA DANIO).
VERTEBRATA; PI
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                                                              PISCES;
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                                                                  GNATHOSTOMATA;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: bular output not generated. Wed Apr 7 09:34:36 1999; MasPar time 26.24 Seconds 856.003 Million cell updates/sec

Title: >US-08-878-177-2 (1-451) from US08878177.pep 3286

Sequence: Description: Perfect Score: 1 MASTIKEALSVVSEDQSLFE.....IYPNTRLPAAHMPSHLGTYY 451

Scoring table: PAM 150 Gap 11

165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 47.907; Variance 81.767; scale 0.586

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Sult No: | Score | Query | Length DB | IĐ | Description | Pred. No. |
|-------------|-------|-------|-----------|--------|------------------------|-----------|
| 1 | 2989 | 91.0 | 478 13 | Q90837 | ERG PROTEIN. | 0.00e+00 |
| N | 1973 | 60.0 | 385 4 | Q14319 | FLI-1. | 0.00e+00 |
| w | 1600 | | 254 4 | Q16199 | EWS-ERG FUSION PROTEIN | 0.00e+00 |
| 4 | 1248 | 38.0 | 196 4 | Q16203 | EWS EWS-ERG=EWS-ER | 1.17e-263 |
| 5 | 730 | 22.2 | 188 5 | Q22355 | MID T | 3.82e-138 |
| თ | 899 | 20.3 | 238 4 | Q99581 | FEV PROTEIN. | 2.08e-123 |
| 7 | 668 | 20.3 | 340 11 | 070132 | ETS DOMAIN TRANSCRIPTI | 2.08e-123 |
| œ | 664 | 20.2 | 208 5 | Q18579 | SIMILARITY TO ETS DOMA | 1.84e-122 |
| 9 | 650 | 19.8 | 336 6 | 062804 | TRANSCRIPTION FACTOR G | 3.78e-119 |
| 10 | 494 | 15.0 | 268 13 | Q91744 | XE1-A DNA-BINDING PROT | 1.14e-82 |
| 11 | 483 | 14.7 | 426 6 | 062803 | TRANSCRIPTION FACTOR E | 3.91e-80 |
| 12 | 483 | 14.7 | 559 5 | Q26645 | ETS HOMOLOGUE. | 3.91e-80 |
| 13 | 451 | 13.7 | 393 5 | 061805 | C. ELEGANS LIN-1 (GB:U | 8.54e-73 |
| 14 | 451 | 13.7 | 441 5 | Q27378 | LIN-1. | 8.54e-73 |
| 15 | 440 | 13.4 | 494 13 | 057586 | ETS-DOMAIN TRANSCRIPTI | 2.76e-70 |
| 16 | 427 | 13.0 | 471 13 | 057566 | TRANSCRIPTION FACTOR G | 2.50e-67 |
| 17 | 366 | 11.1 | 300 11 | 070273 | EHF (EHF). | 1.31e-53 |
| 18 | 348 | 10.6 | 521 4 | Q15725 | NERF-1A. | 1.28e-49 |
| 19 | 348 | 10.6 | 533 4 | Q15724 | NERF-1B. | 1.28e-49 |
| 20 | 348 | 10.6 | 581 4 | Q15723 | ETS TRANSCRIPTION FACT | 1.28e-49 |
| | | | | | | |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | <u>3</u> 5 | 34 | 33 | 32 | 3 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 |
|------------------------|------------------------|------------------------|------------------------|------------------------|--------------|------------|------------------------|------------------------|------------------------|------------------|------------------------|------------------------|--------|--------------------|------------------------|---------|------------------------|------------------------|-------------|------------------------|-------------------|------------------|------------------------|------------------------|
| 224 | 225 | 225 | 225 | 227 | 227 | 227 | 228 | 243 | 245 | 250 | 264 | 262 | 269 | 288 | 307 | 304 | 304 | 304 | 313 | 330 | 336 | 344 | 349 | 349 |
| 6. 8 | • | • | | • | | • | • | | • | • | • | | • | | • | • | • | 9.3 | | • | ٠ | 0 | 10.6 | 10.6 |
| | | | | 98 3 | | | | | | | | | 314 | | | | | 348 | | μ | σ | μ. | | 663 |
| υ | u | σı | U | Ξ | U | σ | Ŋ | G | ω | v | U | σ | IJ | 4 | G | 4 | Ξ | 4 | υı | 4 | 4 | U | 4 | 4 |
| Q25159 | Q23822 | Q25066 | Q25127 | 055199 | 025574 | Q26573 | Q16997 | Q25573 | Q91921 | 044138 | Q93320 | 062767 | 001519 | Q16324 | Q19695 | P78545 | 035275 | Q99718 | 001521 | Q64998 | Q16198 | 017057 | 060435 | Q99607 |
| ETS-1 PROTEIN (FRAGMEN | ETS PROTEIN (FRAGMENT) | ETS-1 PROTEIN (FRAGMEN | ETS-1 PROTEIN (FRAGMEN | ETS TRANSCRIPTION FACT | -2 PROTEIN (| -1 PROTEIN | ETS-2 PROTEIN (FRAGMEN | ETS-1 PROTEIN (FRAGMEN | XRPFIALPHA (FRAGMENT). | C50A2.4 PROTEIN. | HYPOTHETICAL PROTEIN C | ERYTHROBLASTOSIS VIRUS | | TLS ERG {TRANSLOCA | SIMILAR TO DNA BINDING | ESE-1B. | ETS TRANSCRIPTION FACT | EPITHELIAL-SPECIFIC TR | LARITY TP T | (TS1.1 MUTANT) V-ETS (| EWSFLI1 (FRAGMENT | C24A1.2 PROTEIN. | ELF-1 RELATED PROTEIN. | MYELOID ELF-1 LIKE FAC |
| | | | | 8.12e-24 | | | | | | | | | | | | | | 4 | .95e-4 | .17e-4 | 5.63e-47 | .77e- | 7.70e-50 | 7.70e-5 |

ALIGNMENTS

RESULT

| QUEST MACHINES ECONOMIANA QUEST MACHINES QUENCE FROM N.A. TISSUE-SPLEN; MEDLINE; 95329425. DORDAIN P. DEWITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLAUD M.; MEDLINE; 950345; ETS_DOMAIN_1; 1. PROSITE; PSO0345; ETS_DOMAIN_2; 1. PROSITE; PSO0345; ETS_DOMAIN_2; 1. PROSITE; PSO0345; ETS. SEQUENCE 478 AA; 53913 MM; CFE4B9C2 CRC32; QUERY MATCH DUTERQUE-COCUILLAUD M.; MECH. DEV. 50:17-28(1995). EMBL: X77159; G790440; PROSITE; PSO0345; ETS_DOMAIN_2; 1. PROSITE; PSO0345; ETS_DOMAIN_2; 1. PROSITE; PSO0345; ETS. SEQUENCE 478 AA; 53913 MM; CFE4B9C2 CRC32; QUETY MATCH DUTERQUE-COCUILLAUD M.; MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDGSLFECAYGSPHLAKTEMTASSSSETGQTSKMSPRVPQQDWLSQP 1 MASTIKEALSVVSEDGSLFECAYGSPHLAKTEMTASSSSDNYGMYGSYMEEKHIPPPNMTT 1 11 NERRVITENGT NERV NEW | Č | 837 PRELIMINARY; PRT; 478 AA. |
|--|---------|---|
| Ol-NOV-1996 (TREMBLREL OL, CREATED) Ol-NOV-1996 (TREMBLREL OL, LAST SEQUENCE UPDATE) Ol-NOV-1996 (TREMBLREL OL, LAST ANNOTATION UPDATE) ERG. OL-NOV-1996 (TREMBLREL OL, LAST ANNOTATION UPDATE) OL-NOV-1996 (TREMBLREL OL, LAST SEQUENCE SERO, CHORDATA; TETRAPODA; AVES; NEOGNATHAE; OLLIFORMES. [1] SEQUENCE FROM N.A. TISSUE-SEDAN; ETS. DOMAIN_1; 1. PROSITE; PSO0345; ETS.DOMAIN_2; 1. PROSITE; PSO0346; ETS.DOMAIN_2; 1. PROSITE; PSO0346; ETS.DOMAIN_2; 1. PROSITE; PSO0346; ETS.DOMAIN_ | | |
| O1-UN-1998 (TREMBLREL. O6, LAST ANNOTATION UPDATE) ERG PROTEIN. ERG PROTEIN. ERG GALLUS (CHICKEN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAB; GALLIFORMES. [1] SEQUENCE FROM N.A. TISSUE-SPEIEN; MEDLINE; 95329425. DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLADD M.; MECH. DEV. 50:17-28(1995). EMBL; X77159 (790444); PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. | | (TREMBLREI, 01, CREATED) |
| ERG. PROTEIN. ERG. GALLUS (CHICKEN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES. [1] [1] SEQUENCE FROM N.A. TISSUE-SPLEEN; MEDLINE; 9539425. DHORDAIN P. DEWITTE F., DESBIENS X., STEHELIN D., DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00346; ETS_DOMAIN_2; 1. P | | (TREMBLREL. 06, |
| ERG. GALLUS (CHICKEN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES. [1] SEQUENCE FROM N.A. TISSUE-SPLEEN; MEDLINE; 95329425. DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLAUD M.; MECH. DEV. 50:17-28(1995). MECH. DEV. 50:17-28(1995) | | PROTEIN. |
| GALLIUS CALLUS (CHICKEN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES. [1] EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES. [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-SPLEEN; MEDLINE; 95329425. DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLADD M.; MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00346; ETS_DOMAIN_2; 1. PROSITE; PS0 | ERG | |
| EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; [1] [1] [1] [1] [1] [2] [3] [3] [4] [5] [5] [5] [5] [5] [5] [5] [5] [6] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8 | | US GALLUS |
| GALLFORMES. [1] SEQUENCE FROM N.A. TISSUE-SPLEEN; MEDLINE; 95239425. DHORDAIN P., DEWNTTE F., DESBIENS X., STEHELIN D., DUTENOUE-COQUILLAUD M.; MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; PS00412; 1. PROSITE; PS00346; | | TAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; |
| SEQUENCE FROM N.A. TISSUE-SPLEIN; MEDLINE; 95329425 DHORDAIN P., DEWHITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLAUD M.; MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; PTS. PROSITE; PS00440; PTS. PROSITE; PS00440; PTS. PROSITE; PS00440; PTS. PROSITE; PS00440; PTS | | |
| SEQUENCE FROM N.A. TISSUE-SPLEEN; MEDLINE; 95239425. DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., MECH. DEV. 50:17-28(1959). MECH. DEV. 50:17-28(1959). EMBL: X771199; G790440; PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN | | |
| TISSUE-SPLEEN; MEDLINE; 95329425. DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., DHORDAIN P., DEWITTE P., DEWITTE, DEV. 50:17-28(1995). MECH. D., SCOTE 2989; DB 13; Length 478; MECH. D., SCOTE 298; DB 13 | | FROM |
| MEDLINE; 95329425. DHORDAIN P., DEWHITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLADD M.; MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; PS | | SUE=SPLEEN; |
| DHORDAIN P., DEWITTE F., DESBIENS X., STEHELIN D., DUTERQUE-COQUILLAUD M.; MECH. DEV. 50:17-28(1995). MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PROSITE; PS00440; 1. | | |
| DUTERQUE-COQUILLAUD M.; MECH. DEV. 50:17-28(1995). MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PFAM; PF00178; Ets. 91.0%; Score 2989; DB 13; Length 478; Best Local Similarity 94.4%; Pred. No. 0.00e+00; Matches 451; Conservative 0; Mismatches 0; Indels 27; Gaps 1 MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 1 | | F., DESBIENS X., STEHELIN |
| MECH. DEV. 50:17-28(1995). EMBL; X77159; G790440; -:. PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PS00346; ETS_DOMAIN_2; 1. PPAM; PF00178; Etc. PPAM; PF00178; PPAM; PPAM | | |
| EMBL; X77159; G790440; PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PROSITE; PS00345; ETS_DOMAIN_2; 1. PFAM; PF00178; Ets. SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; Query Match 91.0%; Score 2989; DB 13; Length 478; Best Local Similarity 94.4%; Pred. No. 0.00e+00; MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 | | H. DEV. 50:17-28(1995). |
| PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PEAM; PF00178; Ets. SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; Query Match 91.0%; Score 2989; DB 13; Length 478; Best Local Similarity 94.4%; Pred. No. 0.00e+00; MastikealsvvsedQslfecayGsPhlaktemtasssseyGqTskmsprvpQqbwlsQp 60 | | L; X77159; G790440; |
| PROSITE; PS00346; ETS_DOMAIN_2; 1. PFAM; PF00178; ETS. PFAM; PF00178; ETS. SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; Query Match 91.0%; Score 2989; DB 13; Length 478; Best Local Similarity 94.4%; Pred. No. 0.00e+00; MASTIKEALSVYSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 | | PS00345; ETS_DOMAIN_1; |
| PEAM; PEOULNE; ETS. SEQUENCE 478 AA; 53913 MW; CFE4B9C2 CRC32; Sest Local Similarity 94.4%; Pred. No. 0.00e+00; Best Local Similarity 94.4%; Pred. No. 0.00e+00; I MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 I MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 61 PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 | | *O; EIS_DOMAIN_A; |
| Query Match 91.0%; Score 2989; DB 13; Length 478; Best Local Similarity 94.4%; pred. No. 0.00e+00; Matches 451; Conservative 0; Mismatches 0; Indels 27; Gaps 1 MASTIKEALSVYSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 | | AA; 53913 MW; CFE4B9C2 |
| Matches 451; Conservative 0; Mismatches 0; Indels 27; Gaps ASTIKEALSVYSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 | Query I | 91.0%; Score 2989; DB 13; |
| 1 MASTIKEALSVYSEDQSLFECAYGSPHLAKTEMTASSSEYGQTSKMSDRVPQQDWLSQP | Matche | 451; Conservative 0; Mismatches 0; Indels 27; Gaps |
| 1 MASTIKEALSVYSEDQSLFECAYGSPHLAKTEMTASSSEYGGTSKMSPRVPQQDMLSQP 61 PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 61 PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 61 PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 121 NERRVIVPADPTLMSTDHVRQMLEWAVXEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT 61 | | MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP |
| 61 PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKNVSSSDNVGMNYGSYMEEKHIPPPNMTT | | MASTIKEALSVVSEDOSLFECAYGSPHLAKTEMTASSSSEYGOTSKMSPRVPOODWISOP |
| 11111111111111111111111111111111111111 | | TTWINGGGT HERETHAS DANKDANGSSSAMRDDARAGGRANGS DINACINGNACA THAS TO THE TARKET |
| 61 PÄRVTIKMECHPNQVNGSRNSPDDCSVAKGGKMYSSSDNYGMNYGSYMEEKHIPPPNMTT 121 NERRVIVPADPTLMSTDHYRQMLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT | | |
| 121 NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT | | PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT |
| 121 NERRVIVPADETLMSTDHYRQMLEWAYKEYGLPDVDILLEQNIDGKELCKMTKDDFQRIT 181 PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMÄARNTGGATFIFPNTSVYPEA 181 PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMÄARNTGGATFIFPNTSVYPEA 1 | | NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT |
| 181 PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATEIFPNTSVYPEA | | NERRY I VPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT |
| | | PSYNADILLSHLHYLRETPLPHLTSDDVDKALONSPRLMHARNTGGATFIFPNTSVYPFA |
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Best Local S
Matches 25
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Q14319; PRELIMINARY;
Q14319;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0.
01-JUN-1998 (TREMBLREL. 0.
ELI-1.
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HROMAS R., MAY W., DENNY C.,
KLEMSZ M.J.;
RTOCUTY
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EMBL; M93255; G182661; -.
PROSITE: PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
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EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00178; Ets.
SEQUENCE 385 AA; 43437 MW;
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    436
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                                                                                                                                                                                                                                          TESSMYKYPSDISYMPSYHAHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTS-TGGIYPN
                                                                                                                                                            HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTYY
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                                          PNVPRHPNTHVPSHLGSYY 385
                                                                                PESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN
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257; Conser
    RLPAAHMPSHLGTYY
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ilarity 67.8%;
Conservative
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    451
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Pred. No. 0.00e+00;
68; Mismatches 46;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Query Match
Best Local S
Matches 16
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Best Local S
Matches 21
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Q16199 PRELIMINARY; P
Q16199; Q16.199; Q16.199; Q16.1996 (TREMBLREL. 01, CR)
1 01-NOV-1996 (TREMBLREL. 06, L)
1 01-UUN-1998 (TREMBLREL. 06, L)
1 01-UUN-1998 (TREMBLREL. 17/PE 1)
                                       SEQUENCE FROM N.A.

MEDLINE; 94314948.

GIOVANNIXI M., BIEGEL J.A., SERRA M.

GIOVANNIXI M., BIEGEL J.A., SERRA M.

J. CLIN. INVEST. 94:4489-496(1994).

EMBL; S72865; 6533778; --

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PFAM; PF00178; Ets.

NON TER

SEQUENCE 196 AA; 22268 MW; FBCD6
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EMANUEL B.S., EVANS G.A.;
J. CLIN. INVEST. 94:489-496(1994).
EMBL; S72621; G633774; -...
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PFOM; PFO0178; Ets.
                                                                                                                                                                                                              Q16203;
Q16203;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-1998
EWS. EWS-1
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SEQUENCE
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RYOTA; METAZOA; CHORDATA; VERTEBRATA;
ERIA; PRIMATES.
                                                                                                                                                                    SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
ERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                          GSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLS
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                                                                                                                                                                                                                                                                                                                                                                                                 GSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLS
                                                                                                                                                                                                                                                                                                                        KMNEVAPHPPALPVTSSSEFAAPNPYWNSPTGGIYPNTRLPTSHMPSH
                                                                                                                                                                                                                                                                                                              KMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSH
                                                                                                                                                                                                                                                                                                                                                      RALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQ
                                                                                                                                                                                                              7-1996 (TREMBLREL. (
7-1996 (TREMBLREL. (
1-1998 (TREMBLREL. (
.EWS-ERG=EWS-ERG )
Similarity
164; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213; Conservative
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254 AA;
38.0%;
llarity 93.7%;
Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28577 MW;
                                                                                                                                                                                                              01, CREATED)
01, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
FUSION PROTEIN TYPE 9E (FRAGMENT).
Score 1248;
Pred. No. 1.1
7; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1600; DB 4; 1
Pred. No. 0.00e+00;
12; Mismatches 2;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
1E (FRAGMENT).
                                                                                                                            SERRA M.,
                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                                                                                                    PRT;
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                                           FBCD632E
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re 1248; DB 4; L
1. No. 1.17e-263;
Mismatches 4;
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                                                                                                                             WANG
                                                                                                                                                                                                                                                                    196
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                                           CRC32;
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                                                                                                                                                                                 TETRAPODA;
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                                                                                                                             J.Y.,
                    Length 196;
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XX MEDLINE; 94150718.

XX MILSON R., AINSCOUGH R., FAVELLO A., FULTON L., GARDNER A., GREEN P., ALANKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., ALAISTER N., LATISFILLE P., LIGHTNING J., KERSHAW J., ALAISTER N., LATEGILLE P., LIGHTNING J., LAISTER N., LATEGILLE P., LIGHTNING J., PERCY C., ALCOURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., ALCOURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., ALCOURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., THOMAS K., ALCOURRAY A., MOODERS D., SHOWNKEEN R., SMALDON N., SMITH A., ALCOUR M., VAUGHAN K., WATUSTON J., THIERRY-MIEG J., THOMAS K., ALCOUR M., VAUGHAN K., WATUSTON A., WEINSTOCK L., ALCOUR M., WATURE 368:32-38(1994).
                                                                                                                                                                                          Query Match
Best Local S
Matches 9
JLT 6
Q99581
Q99581;
Q99581;
Q1-MAY-1997
Q1-MAY-1997
                                                                                                                                                                                                                                           SUBMITTED (OCT-1995) TO EMBL/GENBAL
EMBL; U39470; G1041871; -
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PFAM; PF00178; Ets.
SEQUENCE 188 AA; 21345 MW; C981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
COSMID T08H4.
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Q22355;
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EUKARYOTA; METAZOA; ACOELOMATES;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                           STELLYES L.;
SUBMITTED (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                        263 DPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARR
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                                                                                     WGERKSKPNMNYDKMSRALRYYYDKNIMAKVHGKRYAYKEDEQGIAQALQP-PTAS
                                                                                                                                                      DPYQILGPTSKNLAHSGSGGTQLWQFLLELLSDKRYSEVITWEGTQGEFKLVDPDEVARK
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                                                                                                                                                                                         h 22.2%;
Similarity 82.8%;
96; Conservative
(TREMBLREL.
                                      PRELIMINARY;
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                                                                                                                                                                                         Score 730; 1
Pred. No. 3.8
8; Mismatcl
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
CREATED)
LAST SEQUENCE UPDATE)
                                      PRT;
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                                                                                                                                                                                                                   DB 5;
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R A., GREEN P.,
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Best Local S
Matches 8
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Best Local S
Matches 8
                                                                Q18579 PRELIMINARY;
Q18579;
Q18579;
Q1. NOV-1996 (TREMBLREL. 01, CF
Q1-NOV-1996 (TREMBLREL. 06, L.
Q1-JUN-1998 (TREMBLREL. 06, L.
C42D8.4.
CAENORHABDITIS ELEGANS
CHERRYOTA; METAZOA; AC
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PROSITE;
SEQUENCE
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATIO
ETS DOMAIN TRANSCRIPTION FACTOR PET-1.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00345: ETS_DOMAIN_1: PROSITE: PS00346: ETS_DOMAIN_2: PFAM: PF00178: Ets.
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EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 98127904.
FYODOROV D., NELSON T., DENERIS
J. NEURODBIOL. 34:151-163(1998).
EMBL; U91679; G3033419; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PETER, COUTURIER J., PACQUEMI MAGDELENAT H., DELATTRE O.; ONCOGENE 14:1159-1164(1997).
EMBL; Y08976; E291921; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     329
                                                                                                                                                                                                                                                                                                            196
                                                                                                                                                                                                                                                                                                                                                         269
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                                                                                                                                                                                                                                                                  GPLSPAVQK-GSGQIQLWQFLLELLADRANAGCIAWEGGHGEFKLTDPDEVARRWGERKS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPNMNYDKLSRALRYYYDKNIMSKVHGKRYAYRFDFQGLAQACQPPPAHA 142
                                                                                                                                                                                                                                                                                                                                                      GPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPES
                                                                                                                                                                                                                                                                                                                                                                                                                                        th 20.3%;
Similarity 77.3%;
85; Conservative
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85; Conser
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PS00346; ETS_DOMAIN_2; 1.
340 AA; 35439 MW; B32
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238 AA;
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77.3%;
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               ACOELOMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25030 MW;
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07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
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                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 668; DB 11;
Pred. No. 2.08e-123;
15; Mismatches 9;
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Pred. No. 2.08e-123;
15; Mismatches 9;
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               NEMATODA; SECERNENTEA; RHABDITIDA.
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                                                                                                                                                                Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O62804 PRELIMINARY; PRT; 336 AA.
062804;
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
TRANSCRIPTION FACTOR GABP ALPHA SUBUNIT (FRAGMENT).
OVIS ARIES (SHEEP).
CUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

EZASHI T., EALY A.D., OSTROWSKI M.C., ROBERTS R.M.;

SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AF057717; G3046690; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD & BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHALDON N., SMITH A SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKLINSON SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U56966; G1293845; -.
PROSITE; PS00346; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PFAM; PF00178; Ets.
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HALLSWORTH K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
        117
                                                            121
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                                                                                   KPNMNYDKLSRALRYYYDKNIMTKVQGKRYAYKFDFQGLAQA 122
-PR--GEILWSHLELLR-K---YVLASQE--QQMNE-IVTI-DQP-VQIIPAS-VQSATP
                                                      NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDF-QRL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKS 328
                                                                                                                                                                      101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368:32-38(1994).
                                                                                                                                                                h 19.8%;
Similarity 41.6%;
101; Conscrvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 20.2%;
Similarity 79.4%;
81; Conservative
                                                                                                                                                                                                                                                                                                                                 PS00345; ETS_DOMAIN_1;
PS00346; ETS_DOMAIN_2;
                                                                                                                                                                                                                                                                                   336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                38033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22664 MW;
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                                                                                                                                                              Score 650; DB 6; Le
Pred. No. 3.78e-119;
61; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 664; DB 5; L
Pred. No. 1.84e-122;
14; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3492097D
                                                                                                                                                                                                                                                                                8CFFE91F
                                                                                                                                                                                                                                                                                CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC32;
                                                                                                                                                                                                                    Length 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 208
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                                                                                                                                                                   Indels
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                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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Best Local Similarity 49.6%;
Matches 66; Conservative
                                                                                                                                                                           O62803 PRELIMINARY; P
O62803; OTREMBLREL. 07, CRE
01-AUG-1998 (TREMBLREL. 07, LAS
01-AUG-1998 (TREMBLREL. 07, LAS
TRANSCRIPTION FACTOR ETS-2 (FRA
OVIS ARIES (SHEEP).
EUKARYOTA; METAADA; CHORDATA; V
EUTHERIA; ARTIODACTYLA.
SEQUENCE FROM N.A.

SZASHI T., EALY A.D., OSTROWSKI M.C., ROBE
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ
EMBL; AF057716; G3046688; -
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-TOTAL OVARY FROM SINGLE FROG;
SALVATI F., MORABITO, MERENDINO, CARNEVALI;
SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ D
EMBL; X65167; G517228; -.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UF
01-AGG-1998 (TREMBLREL. 07, LAST ANNOTATION
XEI-A DNA-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00178; Ets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LELLIDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNFKMNYEKLSRGLRYYYDKNI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDSFDSEDYPP-AMPSHKSKGTFKDYVRDRAELNKDKPVIPAAALAGYTGSGPIQLWQFL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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30805 MW;
                                                                                                                                                                                                                                                            (FRAGMENT).
                                                                                                                                                                                                                                                                                  CREATED)

LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 494; DB 13;
Pred. No. 1.14c-82;
28; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39A1C89D CRC32;
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                                                                                                      ROBERTS
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                                                                                                                                                                                                            TETRAPODA;
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                                                                                                                                                                                                                                                                                       UPDATE)
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                                                                                                   R.M.,
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                                                                                                                                                                                                            MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMPHIBIA;
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Best Local S
Matches 6
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026645;
01-NOV-1996
01-NOV-1996
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          061805;
061805;
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LOYD C., KCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN J
SWALDON N., SMITH A., SONNHAWMER E., STADEN R., SULSTON J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
C. ELEGANS LIN-1 (GB:038937), PARTIAL CDS, CONTAINS
DOMAINS (PPAM: ETS.HMM, SCORE: 162.78).
                                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                   LIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAO S.K., CHILDS G.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ
EMBL; L19541; G310662; -.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PFAM; PFO0178; Ets.
PFAM; PFO0178; Ets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRONGYLOCENTROTUS PURPURATUS (PURPURATUS) EUKARYOTA; METAZOA; ECHINODERMATA;
                                                                                                                                                                                                                                        STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETS HOMOLOGUE
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE~EMBRYONIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUECHINOIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 YEKLSRGLRYYYDKNIIHKTSGKRYVYRF 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 LAGFTGSGPIQLWQFLLELLSDKSCQSFISWTGDGWEFKLADPDEVARRWGKRKNKPKMN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAGYSGSGPIQLWQFLLELLTDKTCQHIISWTGDGWEFKLSDPDEVARRWGKKKKKKKKKKKM 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDKLSRALRYYYDKNIMTKVHGKRYAYKF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEKLSRGLRYYYDKNIIHKTAGKRYYYRF 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDKLSRALRYYYDKNIMTKVHGKRYAYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAN-PGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAN-PGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 14.7%;
Similarity 67.4%;
60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
62; Conse
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5 (TREMBLREL.
8 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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69.7%;
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47795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 483; DB 5;
Pred. No. 3.91e-80;
13; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.91e-80;
10; Mismatches 16
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MATA; ECHINOZOA; ECHINOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0F896532 CRC32;
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                                                                                                                                                                                                                                                                                                                                                          NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Å
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                                                                                                                                                                                                                                                                                                                                                          SECERNENTEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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057586;
01-JUN-1998
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Query Match
Best Local :
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Best Local
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                                                                                                                                                                                                        BEITEL G.J., TUCK S., GREENWALD I. GENES DEV. 9:3149-3162(1995).

EMBL; U38937; G1161370; JOINED.
EMBL; U38936; G1161372; -.

EMBL; U38935; G1161372; -.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    7LT 14
027378
027378;
01-NOV-1996
01-NOV-1996
01-NOV-1998
                                                                                                                                                                   SIGNAL.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF067606; G3158478; -. PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. SEQUENCE 393 AA; 42884 MW; C907FB61 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                             LIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED
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                                                                                                                                                                                              PFAM; PF00178; Ets.
                                                                                                                                                                                                                                                                                                             MEDLINE; 96127909.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLER N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342
 342
                          124 RYYYEKNIIKKVIGKKFVYRF
                                                       283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283
                                                                     64 ITLWQFLLELLQQDQNGDIIEWTRGTDGEFRLIDAEAVARKWGQRKAKPHMNYDKLSRAL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYYYEKNIIKKVIGKKEVYRE
||||:||:||:||:|
RYYYDKNIMTKVHGKRYAYKE
                                                       IQLWQFLLELLSDSSNSNCITWE-GTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRAL
RYYYDKNIMTKVHGKRYAYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A., WEINSTOCK L.
368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%;
Similarity 63.0%;
51; Conservation
                                                                                                             Similarity
51; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                    441 AA;
                                                                                                                                                                                                                                                                                                                                                                   METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL.
(TREMBLREL.
(TREMBLREL.
                                                                                                           13.7%;
larity 63.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                    48227 MW;
                                                                                                                                                                                                                                                                                                                                                                   ACCELOMATES;
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%01,
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                             144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                          Score 451; DB 5; L
Pred. No. 8.54e-73;
17; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 451; DB 5;
Pred. No. 8.54e-73;
17; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                    BC125DF7 CRC32;
                                                                                                                                                                                                                                                                                             Ι.,
                                                                                                                                                                                                                                                                                                                                                                   NEMATODA;
                                                                                                                                                                                                                                                                                              HORVITZ
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                                                                                                                                                                                                                                                                                                                                                                   SECERNENTEA;
                                                                                                                                                                                                                                                                                              H.R.;
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96,

PRT; CREATED)

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Scarch completed: Wed Apr 7 09:36:38 1999 Job time: 122 sccs.
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Best Local Similarity 62.2%;
Matches 51; Conservative
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BROWN L.A., AMORES A., SCHILLING T.F., JOWETT T., BAERT J.L.,

DE LAUNOIT Y., SHARROCKS A.D.;

SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

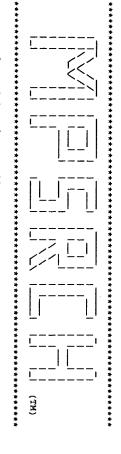
EMBL; AJ7003200; ETS_4815; -.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

SEQUENCE 494 AA; 55620 MW; 249CBBDC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
[1]
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01-AUG-1998 (TREMBLREL: 07, LAST ANNOTATION UPDATE)
ETS_DOMAIN TRANSCRIPTION FACTOR PEA3.
                                                                                                                                                                                                                                                                                  408 LRYYYEKGIMQKVAGERYVYKF 429
                                                                                                                                                                                                                                                                                                                                                                                                                                       341 LRYYYDKNIMTKVHGKRYAYKF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 440; DB 13; Length 494; Pred. No. 2.76e-70; 13; Mismatches 18; Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Sat Apr 10 11:51:41 1999; MasPar time 2419.79 Seconds 1492.252 Million cell updates/sec

bular output not generated.

Title:

>US-08-878-177-3 (1-1528) from US08878177.seq 1528

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 gaattccgcgaacgaataat......gaaagaaagcgccaagaaaa 1528 cttaaggcgcttgcttatta.....ctttctttcgcggttctttt

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 602357 seqs, 1181590623 bases × N

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: emb157

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_vi genbank110

Database:

16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pl2 26:gb_pr1 27:gb_pr2 28:gb_pr3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy 33:gb_un 34:gb_vi

tistics: Mean 11.283; Variance 4.994; scale 2.259

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| G gallus ERG mRNA. Erg 3-immunoglobulin h Human erg2 gene encodi Human erg protein (ets EWSerg (transloca Homo sapiens genomic D EWSEWS-erg-EWS-er Coturnix coturnix mRNA MOUSE Fli-l mRNA for r Sequence 2 from patent H. sapiens HUMFLI-l mRN Fli-l=Friend leukemia | Description |
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| <i>a</i> , | Chicken C-ets-1 oncoge Human DNA for c-ets-1 Sequence 43 from paten Chicken mRNA for c-ets X.laevis mRNA xE1-b fo Chicken protein p54 (e Rat proto-oncogene (Et | p55 (alters) sapiens; sapiens; sophila me sculus crience 3 fre e avian e sculus et | Human FLI-1 mRNA, comp Human ERGB transcripti X.laevis mRNA XLFLI. Homo sapiens FLI-1 gen Sea urchin sequence ho H.sapiens FEV gene, ex H.sapiens mRNA for FEV H.sapiens mRNA for FEV Rattus norvegicus ETS EWS erg {reciproca |
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ALIGNMENTS

| CDS | | gene | | | FEATURES | 000111111 | TITLE | AUTHORS | REFERENCE | MEDLINE | JOURNAL | TITLE | | AUTHORS | REFERENCE | | | | ORGANISM | SOURCE | KEYWORDS | NID | ACCESSION | DEFINITION | Locus | RESULT 1 |
|---|-------------|------------------------------------|---|-----------------------|---------------------------|--|-------|-------------------------|---------------------|----------|--|---|-------------------------|---|---------------------|-----------------------------------|---|--|---------------|----------|-----------|---------|-----------|---------------|-----------------------------------|----------|
| 631499 /gene="ERG" /codon_start=1 /db_xref="PID:g790440" | /gene="ERG" | /clone_lib="lambda gt10" 631499 | /dev_stage="adult" /tissue_type="spleen" | /db_xref="taxon:9031" | Location/Qualifiers 11516 | Oncologie Moleculaire, Institut Pasteur, 1 rue Calmette, 59019 | | Duterque-Coquillaud, M. | 2 (bases 1 to 1516) | 95329425 | Precarcing industry and carcinge differentiation mech. Dev. 50 (1), 17-28 (1995) | Mesodermal expression of the chicken erg gene associated with | Duterque-Coquillaud, M. | Dhordain, P., Dewitte, F., Desbiens, X., Stehelin, D. and | 1 (bases 1 to 1516) | Phasianidae; Phasianinae; Gallus. | Vertebrata; Archosauria; Aves; Neognathae; Galliformes; | Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; | Gallus gallus | chicken. | ERG gene. | 9790439 | x77159 | lus ERG mRNA. | GGERG 1516 bp RNA VRT 27-APR-1995 | |

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MHARNTGGATFIFPNTSYYPEATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPS
STYPKTEDQRPQLDPYQILGPTSSRLANPGSGGIQLWQFLLELLSDSSNSNCITWEGT
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(alternatively spliced) [mice, pr
816 nt].
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GenBank staff at the
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                                                                                          Rivera, R.R., Stuiver, M.H., Ets proteins: new factors 1
                                                                                                                                              Mus sp.
Eukaryotae;
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                              [NCBI gibbsq 138523] sequence comes from F
                                                                                                                                                                 pre-B-cell line
         Location/Qualifiers
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/organism-"Mus
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                                                                       Biol.
                                                                                                                                   Eutheria;
                                                                                                                                              mitochondrial eukaryotes; Metazoa;
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in enhancer-binding Ets protein
pre-B-cell line 22D6, mRNA Par
                                          the
                                                                                                                                   Sciurognathi;
                                        original journal article
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Muridae; M
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                                                                                         GACAAAAACATCATGACCAAGGTGCACGGGAAGCGCTACGCCTACAAGTTTGACTTCCAC
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                                                                                                                                      AGGAAGAGCAAGCCCAACATGAACTATGACAAGCTCAGCCGCGCGCCCTCCGCTACTACTAC
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/translation="DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPR
/translation="DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPR
LMHARNYGGAAFIFPNTSYYPEATQRITTRPDLPYEPPRRSAWFGHSHLTPQSKAAQP
SPSAVEKTEDQRPQLDPYQILGPTSSKLANPGSGQIQLWQFTLELLSDSSNSNCITWE
GTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFD
FHGIAQALQPHPPESSLYKXPSDLPYMGSYHAHPQKMNFVSPHPPALPVTSSF"
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/note-"immunoglobulin heavy-chain enhancer-binding Ets
protein"
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/gene="Erg-3"
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CACCATCAAAATGGAATGTAACCCTAGCCAGGTGAATGGCTCAAGGAACTCTCCTGATGA
                                                  atcgccccaccttgcaaagacagaaatgacagcctcctcttccagtgaatatgggcaaac 193
                                                                                                              AACGCCACACCTGGCTAAGACAGAGATGACCGCGTCCTCCTCCAGCGACTATGGACAGAC
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                               atcaaagatgagcccgcgcgttccccagcaggactggttatcacagcccccggccagagt
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M17254
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257. .1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GDB:G00-119-884"
/db_xref="PID:g182187"
/db_xref="PID:g182187"
/db_xref="PID:g182187"
/translation="MIDPONTENTIAL SUVSEDQSLFECAYGTPHLAKTEMTASS
SSDYGOTSKMSPRVPQQDWLSQPPARVTIKMECNPSQVNGSRNSPDECSVAKGGKNVG
SPDTVGMNYGSYMEEKHMPPPNMTTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLP
DVNILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKA
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257. .1645
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/db_xref="taxon:9606"
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ne encoding erg2
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Pred. No. 0.00e+00;
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The erg gene: A human gene related to the ets oncogene Proc. Natl. Acad. Sci. U.S.A. 84, 6131-6135 (1987)
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PSTVPKTEDQPDEVARRWGERKSKPNMNYDKLSRALRYXYDKNIMTKVHGKRYAYKFDF
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Giovannini,M., Biegel,J.A., Serra,M., Wang,J.Y., Wei,Y.H., Mycum,L., Emanuel,B.S. and Evans,G.A.
EWS-erg and EWS-Fill fusion transcripts in Ewing's sarcoma an primitive neuroectodermal tumors with variant translocations J.Clin. Invest. 94 (2), 489-496 (1994)
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/noten"fusion gene"
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                                           /product-"EWS-erg fusion protein type 1e"
/db_xref-"pID:9633774"
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/translation-"PTSYPPOTGSYSQAPSQYSQQSSSYGQQNLPYEPPRRSAWTGHG
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DSSNSSCITWEGTNGEFKMTDDDEVARRWGERKSKPNNNYDKLERALRYYYDKNIMTK
VHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPAL
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/gene-"EWS-erg"
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Hirakawa,M., Yamaguchi,H. and Imai,K.

Homo sapience 1,296,826bp genomic DNA of 21q22.2 Do
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Eukaryotas; mitochondrial cukaryotes; Metazoa; Vertebrata; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 588) Giovannini,M., Biegel,J.A., Serra,M., Wang,J.Y. Nycum,L., Emanuel,B.S. and Evans,G.A. EWS-erg and EWS-Fli1 fusion transcripts in Ewir primitive neurocctodermal tumors with variant t
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Direct Submission
Submitted (11-MAY-1998) to the DDBJ/EMBL/GenBank databases. Mika
Submitted (11-MAY-1998) to the DDBJ/EMBL/GenBank databases. Mika
Hirakawa, Japan Science and Technology Corporation (JST), Advance
Databases Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo, Tokyo
102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491)
Fax:81-3-5214-8470)
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438; Conservative
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.EWS-erg-EWS-erg fusion protein type 9e
.RNA Partial Mutant, 3 genes, 588 nt].
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/db_xref="taxon:9606"
/chromosome="21"
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29023 c 28295 g
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Pred. No. 2.06e-294;
0; Mismatches 85;
                                    Serra, M., Wang, J.Y.,
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                                     Wei, Y.H.,
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             sarcoma
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                                            atgaactitgtagctccccatccccctgctttgcccgtaacctcatccagcttttttgct
                                                                                                               ATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCCGTGACATCTTCCAGTTTTTTTGCT
                                                                                                                                                                                                                                                                                        GCCCGGCCTGGGGAGAGCGGAAGAGCAAACCCAACATGAACTACGATAAGCTCAGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACGGATCCCGACGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agtgggcagatacagctatggcagttcctactggagcttctgtcggacagctccaactcc 1040
ACCAGCCATATGCCTTCTCAT
                             gcccctaatccatactggaattcaccaactggaggcatctaccccaataccaggctgcca
                                                                                                                                                                                                                                                                                                                               GCCCTCCGTTACTACTATGACAAGAACATCATGACCAAGGTCCATGGGAAGCGCTACGCC
                                                                                                                                                                                                                                                                                                                                                            gctcggcgttggggagagaggaaaagcaaacctaacatgaactatgacaaactcagccgt
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94314948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created thientry (NCBI gibbsq 154042) from the original journal article. This sequence comes from Fig. 2A.

Location/Qualifiers
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llarity 83.6%;
Conservative
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/translation="PTSYPPOTGSYSQAPSQYSQQSSSYGQOSSGQIQLWQFLLELLS
/translation="PTSYPPOTGSYSQAPSQYSQQSSSYGQOSSGQIQLWQFLLELLS
DSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNIMTK
VHGKRYAYKDDHGIAGALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPAL
PVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSH"
210 c 129 g 104 t
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/gene-"erg"
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/notee"EWS-erg fusion
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/gene="EWS-erg"
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/db_xref="taxon:9606"
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d. No. 3.32e-279;
Mismatches 82;
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                                                                                                                                                                                   TCTTGCCAATCCTGGGAGTGGGCAGATACAACTGTGGCAGTTCCTCCTCGAGTTGCTGTC 1029
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                     AGACCCAGATGAAGTGGCACGGCGCTGGGGAGAACGCAAAAGCCAAGCCCAACATGAATTA 1149
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agaccctgatgaagtggctcggcgttggggagagagggaaaagcaaacctaacatgaacta
                                                                               ggacagctccaactccaactgcatcacctgggaggcacaaatggggagttcaagatgac
                                                                                                                          GGACAGTTCCAATGCCAGCTGTATCACATGGGAAGGGACCAATGGGGAATTCAAGATGAC
                                                                                                                                                               tcttgcaaatccagggagtgggcagatacagctatggcagttcctactggagcttctgtc
                                                                                                                                                                                                                                                 rıı gene;
quail.
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The avian fil gene is specifically expressed during embryogenesis in a subset of neural crest cells giving rise to mesenchyme Int. J. Dev. Biol. 42 (4), 561-572 (1998)
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Coturnix coturnix mRNA for
Y14773
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Direct Submission

Direct Submission

Submitted (09-SEP-1997) P. Stiegler, Centre National de Recherche, Scientifique, U.P.R. 9005 du C.N.R.S, 15 Rue Descartes, 67084 Strasbourg Cedex, FRANCE

Related sequence Y14774.
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Neognathae; Galliformes; Phasianidae; Phasianinae; Cott
1 (bases 1 to 3490)
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/function="transcription factor"
/function="transcription factor"
/codon_start=1
/product="FLI transcription factor"
/product="FLI transcription factor"
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/db_xref="PID:g1308265"
/db_xref="PID:g13269303"
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PHKINPLPPQQEWINQPVRVNVKREYDHMNGSRESPVDCSVNKCSKLVGAGTESNPMS
YSTYNDEKNGFPPNMTINERRYLVPADPTLWTQCHYROWLEWAIKEYGLMEIDTTFFQ
NMDGKELCKMNKDDFLRTTSLXNTEVLLSHLSYLRESSSLLAYXYFSHTEASSRLATK
EGPPVAGTQNVNKTTEQQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSN
ASCITWEGTNGEEKMTDPDEVARRWGERKSKPNNYDKLSRALRYYYDKHIEKTKVHGK
ASCITWEGTNGEEKMTDPDEVARRWGERKSKPNNYDKLSRALRYYYDKHIEKTKVHGK
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215. .1
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SSFFGAASPYWTSPAGSIYPNPNVPRHPNAHVSPHLGSYY"
1770 c 752 g 942 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="4-day quail embryo"
/clone_lib="pCDNAI"
/clone="10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism~"Coturnix coturnix"
/db_xref~"taxon:9091"
/chromosome~"1"
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                                                                                                                                                                                                                                                                                                                                 Score 320; DB 21; I
Pred. No. 4.49e-263;
0; Mismatches 114;
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SI, clone 10.1.
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1 (bases 1 to 3545)

Mager,A.M., Grapin-Botton,A., Ladjali,K., Meyer,D., Wolff,C.M., Stiegler,P., Bonnin,M.A. and Remy,P.

The avian fil gene is specifically expressed during embryogenesis in a subset of neural crest cells giving rise to mesenchyme

Int. J. Dev. Biol. 42 (4), 561-572 (1998)
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Coturnix coturnix
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Y14774
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/product="FLI transcription factor<"
/db_xref="FLI :e1308263"
/db_xref="FLI :e1308263"
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ERSYSTLAYNTPSHTEASSKLATKEGFPVAGTQNVNKTTEQQRPQPDDYQILGPTSS
RLANPGSGQIQLMQFLLELLSDSSNASCITWEGTNGEFKMTDPDEVARRWGERKSKPN
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396. .1595
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396. .1595
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/chromosome="1"
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/clone_lib="pCDNAI"
/clone="6.1"
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/function="transcription
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                                                                                                                                                                                                g50974
c-ets-1 gene;
house mouse.
Letwin, K.

Direct Submission

Direct Submission

Submitted (08-MAY-1991) K. Letwin, Samuel Lunenfeld Res

Mount Sinai Hospital, Div of Mol and Developmental Biol,

University Avenue, Toronto Ontario M5G 1X5, CANADA

2 (bases 1 to 1729)

Ben-David, Y., Giddens, E.B., Letwin, K. and Bernstein, A.
                                                                                                                                                                                                                                             Mouse Fli-1 mRNA for X59421
                                                                                                                                                    Eukaryotae; mitochondrial
Vertebrata; Eutheria; Rode
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/gene-"fil"
/note-"FTS binding d
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MPSYHAHQQKVNFVPPHPSSMPVTSSSFFGAASPYWTSPAGSIYPNPNVPRHPNAHVS
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Pred. No. 3.53e-261;
0; Mismatches 115;
                                                                                                                                                   rial eukaryotes; Metazoa; Chordata; Rodentia; Sciurognathi; Myomorpha;
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                                                                                  CAACAGAAGGTGAACTTTGTCCCGTCTCACCCATCCTCCATGCCTGTCACCTCCTCCAGC 1486
                                                                                                                                                                                                                                                                                                                                  AGGTATGCCTACAAGTTTGACTTCCATGGCATTGCCCAGGCCCTGCAGCCCACATCCAACA 1366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tccaactccaactgcatcacctgggaggcacaaatggggagttcaagatgacagaccct
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TTCTTTGGAGCAGCATCACAATACTGGACCTCCCCCACTGCTGGGATCTATCCAAACCCC
                                                                                                                                                                          gaatcatccatgtacaaatacccatcagacctcccctacatgagttcctaccatgcacac 1331
                                                                                                                                                                                                                                          GAGACATCCATGTACAAGTATCCCTCTGATATCTCCTACATGCCTTCCTACCATGCCCAT 1426
                                                                                                                                                                                                                                                                                                  cgctatgcctacaaatttgatttccacggaatcgctcaggccttccagcctcca
                                                                                                                                                                                                                                                                                                                                                                                                                           ctcagccgtgcacttcgctactactatgacaaaaatattatgactaaagttcatggtaaa
                                                     ccccagaagatgaactttgtagctccccatcccctgctttgcccgtaacctcatccagc
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/codon_start=1
/product="retrovirus integration site"
/product="retrovirus integration site"
/product="spid:g50975"
/db_xref="spid:g50975"
/db_xre
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LSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTETSMYKYPSDISYMPSYH
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/strain="balb/c"
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Pred. No. 2.78e-259;
0; Mismatches 113;
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                                                                                                                                                                                                                                                                                                            1031 ctccaactccaactgcatcacctgggagggcacaaatggggagttcaagatgacagaccc
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Local Similarity 78.8%;
hes 427; Conservative
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             CGAGTCGTCCATGTACAAGTACCCTTCTGACATCTCCTACATGCCTTCCTACCATGCCCA
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Other
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NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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publication JP 8500964T 960206.
Location/Qualifiers
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/db_xref="taxon:9606"
/dev_stage="ADULTE"
686 c 663 g 72
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om Patent W09323549
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Pred. No. 1.71e-255;
0; Mismatches 115;
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Watches 427; Conserv
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X67001 S44250
g32529
FLI-1 gene homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene fusion with an ETS DNA-binding translocation in human tumours Nature 359 (6391), 162-165 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peter,M., Kovar,H., Joubert,I., de Jon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-MAY-1992) O. Delattre, Lab. de (Inst. Curie, 26 rue D'Ulm, 75231 Paris Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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/product="homologue of the murine fli-1 gene"
/product="homologue of the murine fli-1
/product="homologue of the fli-1
/db_xref="piD:g32530"
/db_xref="piD:g32530"
/db_xref="sWIS--PROT:001543"
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NMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLRESSLLAYNTTSHTDQSSRLSVKE
DPSYDSVRRGAMGNNNNSGLNKSPFLGGAQTISKNTEQRPQPDFYQILGFTSSRLANP
GSGQIQLWQFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSPDNSYNMSYH
LSRALRYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHFTESSMYXYPSDLSYMPSYH
LSRALRYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHFTESSMYXYPSDLSYMPSYH
AHQQKVNFVPPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGS
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/db_xref="taxon:9606"
/dev_stage="adult"
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Location/Qualifiers
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Prasad,D.D., Rao,V.N. and Reddy,E.S.
Structure and expression of human Fli-1 gene Cancer Res. 52 (20), 5833-5837 (1992)
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/notes"Friend
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134. .1492
                                                                                                                                                      /organism="Homo sapiens"
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134. .1492
/db_xref~"PID:g257354"
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Human FLI-1 localizes to chromosome 11024 and has an abcrrant
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NMDGKELCKMNKEDFLRATTLY NTEVLLSHLSYLRESSLLAY NTTSHTDQSSRLSVKE
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1406 AAGATATGCTTACAAATTTGACTTCCACGGCATTGCCCAGGCTCTGCAGCCACATCCGAC 1465
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Local Similarity 79.0%;
hes 402; Conservative
                                                                                                                                                                                                                                                                                                                                                                      CAACCCTGGAAGCGGGCAGATCCAGCTGTGGCAATTCCTCCTGGAGCTGCTCTCCGACAG 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCAACGCCAGCTGTATCACCTGGGAGGGGACCAACGGGGAGTTCAAAATGACGGACCC 1285
                                              actcagccgtgcacttcgctactactatgacaaaaatattatgactaaagttcatggtaa 1210
                                                                                            GCTGAGCCGGGCCCTCCGTTATTACTATGATAAAAACATTATGACCAAAGTGCACGGCAA 1405
                                                                                                                                                                                                                                              ctccaactccaactgcatcacctgggagggcacaaatggggagttcaagatgacagaccc 1090
                                                                                                                                                                                                                                                                                                                                             aaatccagggagtgggcagatacagctatggcagttcctactggagcttctgtcggacag
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93176799
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join(1. 401,576. .1932)
/gene="FLI-1"
join(174. 401,576. .1700)
/gene="FLI-1"
/note: "alternate"
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/Product-"FLI-1"
/Product-"FLI-1"
/Ab_xref-"PID:9182661"
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KMNKEDFLRATTLYNTEVLLSHLSYLRESSLLAYNTTSHTDQSSRLSVKEDPSYDSVR
RGAWGNNNNSGLMKSPPLGGAQTISKNTEQDRPQDPYQILGFTSRLANPGSGQIQLW
QFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGKENMNYDKLSRALRYY
YDKNIMTKVHGKRYAYKDFHGLAGALQPHPTESSMYKYPSDLSYMPSYHAHQQKVNF
VPPHPESMPVTSSSFFGAASQYWTSTGGIYPNPNVPRHPNTHVPSHLGSYY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQ
PHKINFLPRQOEWINQPYRVNVKRYDHNNGSESPVDCSVSKCSKLYGGGESRPNNN
SYMDEKNGPPP PNMTINERRYLFVBADATLYTGEBYRQNLEMAIKEYSLHEIDTSFFQN
MDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLBESSLLAYNTTSHTDQSSRLSVKED
PSYDSYRRGANGNIMTKVHGKTYDKHESFKLTDREGFKNTDPGPADFYQILGPTSSRLANPG
SGQIQLWQFLLELLSDSAANSKFDFHGIAAKFFDFHGIAALQPHFTESSHKYEPSDSAANSTDKL
SRALRYYYDKHIMTKVHGKRYAKKFDFHGIAACFKNTDPGPADFYQILGPTSSNMNYDKL
SRALRYYYDKHIMTKVHGAKKYAKKFDFHGIAACFKNTDPGPADFYQILGPTSSNMNYDKL
SRALRYYYDKHIMTKVHGAKYAKKFDFHGIAACFKNTDPGPADFYQILGPTSSNMNYDKL
SRALRYYYDKHIMTKVHGAKYAKFDFHGIAACFKNTDPGPADFYQHDYNPRHPNTHYPSHLGSYY
HQQKVNFYPPHPSSMPVTSSSFFGAASQYWTSTGGIYPNPNVPRHPNTHYPSHLGSYY
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/note="alternate"
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/gene="FLI-1"
/note="alternate"
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/db_xref="taxon:9606"
/cell_line="HEL"
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/map="11q23-25"
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/tissue_type="blood"
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Pred. No. 2.08e-239;
0; Mismatches 107;
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Best Local S
Matches 40
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ctccaactccaactgcatcacctgggagggcacaaatggggagttcaagatgacagaccc
                               CGCCAACGCCAGCTGTATCACCTGGGAGGGGACCAACGGGGAGTTCAAAATGACGGACCC 1113
                                                                                                                                                                                                 CAACCCTGGAAGCGGCCAGATCCAGCTGTGGCAATTCCTCCTGGAGCTGCTCTCCGACAG 1053
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1 (bases 1 to 2954)
Watson, D.K., Smyth, F.E., Thompso
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The ERGB/FIII gene: Isolation and characterization of the family of human ETS transcription factors Cell Growth Differ. 3, 705-713 (1992)
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Similarity 78.8%;
401; Conservative
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Vertebrata; Eutheria; Primates; Catarrhini; Hor
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Human ERGB
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LSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSQH
AHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSTGGIYPNPNVPRHPNTHVPSHLGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product "ERGS transcription factor"
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/translation="MDGTIREALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQ
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NMDGKELCKHNKKEDFLRATTLXNTEVLLSHLGSVLRESSLAYNTTSHTDQSSRLSVK
DPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANP
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/db_xref="taxon:9606"
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transcription
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s (library: lambda gtl0) cDNA t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2940
8 c
                                                                                                                                                                                                                                                                                                                                                                                               Score 293; DB 26;
Pred. No. 1.62e-237;
0; Mismatches 108:
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n factor (FLI-1 homolog) mRNA,
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 1391
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                                          1234 AAGATATGCTTACAAATTTGACTTCCACGGCATTGCCCAGGCTCTGCAGCCACATCCGAC 1293
                                                                                                                  CTTCTTTGGAGCCGCATCACAATACTGGA 1442
                     tgatgaagtggctcggcgttggggagagagggaaaagcaaacctaacatgaactatgacaa 1150
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Search completed: Sat Apr 10 12:38:54 1999 Job time : 2833 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 7 09:43:13 1999; MasPar time 20.29 Seconds $882.246\ Million\ cell\ updates/sec$

bular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-878-177-4
(1-478) from US08878177.pep
1 MASTIKEALSVVSEDQSLFE.....IYPNTRLPAAHMPSHLGTYY 478

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 48.417; Variance 93.758; scale 0.516

SUMMARIES

| Sult No. | Score | % Query Match | Length | DB G | ID | Description | Pred. No. |
|-------------|-------|---------------------|--------|---|--------|-----------------------|-----------|
| 1 | 3126 | | 478 | ے ا | S60754 | transcription factor | 0.00e+00 |
| 2 | 3032 | 87.5 | 486 | ш | TVHUEG | 'n | • |
| ω | 1776 | | 452 | ب | I37565 | | |
| 4 | 1773 | | 452 | <u>, , , , , , , , , , , , , , , , , , , </u> | S17403 | | |
| 5 | 1740 | | 453 | ب | S49013 | | |
| თ | 1571 | | 272 | N | A54617 | - | |
| 7 | 1401 | | 385 | _ | S29844 | transforming protein | 5.17e-265 |
| 8 | 745 | | 173 | N | A56646 | - | |
| ம | 691 | | 179 | N | S51226 | transcription factor | |
| 10 | 519 | | 103 | N | S28823 | transcription factor | .57e- |
| 11 | 467 | | 94 | N | S28820 | transcription factor | |
| 12 | 458 | | 268 | N | S11224 | transcription factor | .80e- |
| 13 | 458 | • | 438 | Ь | S11225 | transcription factor | .80e- |
| 14 | 456 | • | 440 | _ | A35875 | transcription factor | .60e- |
| 15 | 456 | • | 441 | Н | A53988 | transcription factor | .60e- |
| 16 | 456 | | 441 | Ь | TVHUET | transcription factor | 9.60e-65 |
| 17 | 453 | | 472 | ш | в53236 | transcription factor | .86e- |
| 18 | 452 | • | 211 | N | S24300 | transforming protein | .14e- |
| 19 | 451 | | 440 | N | I48291 | 3 | .76e- |
| 20 | 452 | | 441 | <u> </u> | TVCHTE | | .14e- |
| 21 | 452 | | 454 | , | A48146 | GA-binding protein al | .14e- |
| 22 | 452 | | 454 | ۱ | A40858 | protein | .14e- |
| 23 | 451 | 13.0 | 454 | N | I38739 | spiratory | .76e- |
| | | | | | | | |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
|-----------------------|----------------------|----------------|----------|----------|-----------------------|----------------------|-----------------------|----------|----------|----------|------------|---------|-----------------------|----------|----------|----------|----------|----------|----------------------|----------------------|----------------------|
| 383 | 393 | 394 | 395 | 395 | 397 | 407 | 407 | 404 | 419 | 425 | 425 | 434 | 434 | 440 | 445 | 445 | 448 | 447 | 452 | 450 | 452 |
| 11.0 | 11.3 | 11.4 | 11.4 | 11.4 | 11.5 | 11.7 | 11.7 | 11.7 | 12.1 | 12.3 | 12.3 | 12.5 | 12.5 | 12.7 | 12.8 | 12.8 | 12.9 | 12.9 | 13.0 | 13.0 | 13.U |
| 453 | 250 | 430 | 429 | 428 | 548 | 555 | 462 | 342 | 510 | 477 | 477 | 718 | 623 | 110 | 469 | 468 | 488 | 479 | 485 | 472 | 464 |
| N | N | N | N | μ | N | щ | μ | N | ۳ | Н | 1-1 | ب | ۳ | N | ب | _ | μ | ب | ب | ۲ | ۲ |
| B42093 | A54308 | I48755 | JC4965 | TVHUEK | S59133 | S24061 | S35534 | A46396 | S43692 | I38893 | B46396 | S33168 | S33167 | A45938 | TVHUE2 | TVMSE2 | TVFVES | TVCHE2 | TVCHET | A53236 | 53/616 |
| serum response factor | PE-1 protein - human | mSAP1a - mouse | - mouse | | ETS2 repressor factor | transcription factor | adenovirus ElA enhanc | 7 | factor | factor | | spli | pointed protein, spli | factor | | factor | factor | factor | transcription factor | transcription factor | transcription lactor |
| 3.51e-50 | 3.71e-52 | 2.35e-57 | 1.49e-52 | 1.49e-52 | 5.99e-53 | 6.20e-55 | 6.20e-55 | 2.45e-54 | 2.53e-57 | 1.60e-58 | 1.60e-58 | 2.53e-6 | 2.53e-60 | 1.59e-61 | 1.57e-62 | 1.57e-62 | 3.92e-63 | 6.22e-63 | 6.14e-64 | 1.55e-63 | 6.14e-64 |

ALIGNMENTS

| Db 121 NERRVI Qy 121 NERRVI | Db 61 PARVTI Qy 61 PARVTI | Db 1 MASTIK Qy 1 MASTIK | Query Match Best Local Sim Matches 441; | 119-193 312-390 SUMMARY | #gene CLASSIFICATION KEYWORDS | -1 -1 | #cross-refere | #journal #title | ACCESSIONS REFERENCE #authors | RESULT 1 ENTRY TITLE ORGANISM DATE |
|--|--|---|--|--|--|--|--|--|--|---|
| NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT 180 | PARVTIKMECNPNQVNGSRNSPDDCSVÅKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 | MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP 60 | Query Match 90.2%; Score 3126; DB 1; Length 478; Best Local Similarity 92.1%; Pred. No. 0.00e+00; Matches 441; Conservative 10; Mismatches 26; Indels 2; Gaps 2; | #domain ets RII regulatory region homology #label ETS2\ #domain ets DNA-binding domain homology #label ETS #length 478 #molecular-weight 53913 #checksum 547 | erg #superfamily transcription factor erg; ets DNA-binding domain homology; ets RII regulatory region homology DNA binding; phosphoprotein; proto-oncogene; transcription factor; transforming protein | ##status preliminary ##molecule_type mRNA ##rosidues 1-478 ##label DHO ##cross-references EMBL:X77159; NID:g790439; PID:g790440 | precartilaginous condensation and cartilage differentiation. cross-references MUID:95329425 accession S60754 | Duterque-Coquillaud, M. Mech. Dev. (1995) 50:17-28 Mesodermal expression of the chicken erg gene associated with | S60754 S60754 Dhordain, P.; Dewitte, F.; Desbiens, X.; Stehelin, D.; | \$60754 *type complete transcription factor erg - chicken frommal_name Gallus gallus *common_name chicken 27-Apr-1996 *sequence_revision 23-May-1997 *text_change 10-Jul-1998 |

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TITLE
CONTAINS
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                       #cross-references MUID: 94119611
#accession I58410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Reddy, E.S.P.; Rao, V.N.; Papas, T.S.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6131-6135
#title The erg gene: a human gene related to the ets oncogene.
#cross-references MUID:87317608
                                                                                  1-231,256-486
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                                                                                                                                                                                                                                                                                     ##status preliminary; translated
##molecule_type mRNA
##residues 230-259 ##label RES
##cross-references GB:S68130; NID:954496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
#residues 1-231,256-486 ##label REA
##cross-references GB:M17254; NID:g182186;
                                                                                                                                                                                                      ##cross-references GDB:119884; OMIM:165080 p_position 21q22.2-21q22.2
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                                                                                                                  #superfamily transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology
alternative splicing; DNA binding; nucleus; proto-oncogene;
transcription factor; transforming protein
                                                                                                                                                                                                                                                 GDB: ERG
                                                                                                                                                                                                                                                                                                                                                                                                             Prasad, D.D.; Rao, V.N.; Lee, L.; Rec Oncogene (1994) 9:669-673
Differentially spliced erg-3 product transcriptional activator.
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transforming protein erg-1; transforming protein erg-2
#formal_name Homo sapiens #common_name man
31-Mar-1989 #sequence_revision 30-May-1997 #text_change
31-oct-1997
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                   #product transforming proitein erg-2 #status predicted
#label EGQ\
#product transforming protein erg-1 #status predicted
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Best Local
#accession S29843
##molecule_type mRNA
1-68'v',70-129,'A',131-132,'V',134-322,'Q',324-425,
##residues 427-452 ##label HRO1
                                                                                                                                                                                                                                                                                                      #journal #title
                                                                                                                  #journal
#title
                                                                    #cross-references MUID:93176799
#accession S29843
                                                                                                                                                                                                                                                        #cross-references MU
#accession I37565
                                                                                                                                                                                                                                                                                                                                                                 #authors
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NCE S29843
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Similarity 87.5%;
419; Conservative
                                                                                               Hromas, R.; May, W.; Denny, C.; Raskind, W.; R.A.; Beck, E.; Klemsz, M.J.
Biochim. Biophys. Acta (1993) 1172:155-158
Human FLI-1 localizes to chromosome 11024 and transcript in neuroepithelioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transforming protein fil, long splice form - human Friend leukemia integration protein 1; transcription
                                                                                                                                                                                                                                                                                        Gene fusion with an ETS DNA-binding chromosome translocation in human
                                                                                                                                                                                                                                                                                                                   T.; Peter, M.; Kovar, H.; Joubert, Rouleau, G.; Aurias, A.; Thomas, G. Nature (1992) 3599:162-165
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#length 486
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04-Oct-1996 #sequence_revision 30-May-1997 #text_change
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                                                                                                                                                                                                                                                                    chromosome translocation in s MUID: 92396239
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Pred. No. 0.00e+00;
28; Mismatches 29
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ht 54608 #checksum 9577
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Best Local Similarity 57.4%;
Matches 278; Conservative
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p_position llg24.1-llg24.3
                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
##residues 1-6 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-390,'Q',392-425,427-452 ##label WAT ##cross-references GB:M98833; NID:g182188; PID:g182189 ##note sequence extracted from NCBI backbone
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##cross-references GB:S45205; NID:g257353; PI
##note sequence extracted from NCBI
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1-68, V',70-76,78-129,'A',131-132,'V',134-322,'Q'
##residues 324-425,427-452 ##label HRO2
324-425,427-452 ##label HRO2
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1 MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQPHKINPLPPQQEWINQ 60
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Human FLI-1, an ETS oncogene family member preferentially expressed in hematopoetic cells, is a sequence-specific
                                                                                                                                                                                           #superfamily transcription factor erg; ets DNA-binding domain homology; ets RII regulatory region homology alternative splicing; DNA binding; nucleus; proto-oncogene; transcription factor; transforming protein
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The ERGB/Fil-1 gene: isolation and characterization member of the family of human ETS transcription for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watson, D.K.; Smyth, F.E.; Thompson,
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                                                                                                                #domain ets RII regulatory region homology #label : #domain ets DNA-binding domain homology #label ETS #length 452 #molecular-weight 50982 #checksum 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The human homolog of the mouse common viral region, FLI1 maps to 11q23-q24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics (1991) 11:223-224
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                                       86;
                                                        Score 1776; DB 1; Pred. No. 0.00e+00;
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59; PID:g182660
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                                                     Query Match
Best Local S
Matches 27
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insertional activation of a new member of the ets gene
#cross-references MUID:91257578
##molecular insertional activation of a sew member of the ets gene
#cross-references MUID:91257578
                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
#residues 1-452 ##label
##cross-references GB:X59421;
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1 MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQPHKINPLPPQQEWINQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNYDKLSRALRYYYDKNIMTKVHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDFHGIAQA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYP-SDISYM 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TINERRVIVPADPILWIQEHVRQWLEWAIKEYSLMEIDISFFQNMDGKELCKMNKEDFLR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-VRVNVKREYD--HMNGSRESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNM 117
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                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Mus musculus #common_name house mouse 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Sep-1997
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Friend leuken
                                                                                                                       #length 452
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                                                     Conservative
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#domain ets DNA-binding domain homology #label ETS
#th 452 #molecular-weight 51002 #checksum 8905
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                                                                     51.1%;
57.2%;
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                                                   Score 1773; DB 1; Pred. No. 0.00e+00; 89; Mismatches 80;
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                                         Query Match 50.2%;
Best Local Similarity 56.4%;
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                              #journal #title
                                                                                                                                                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                          ##molecule_type mRNA
##residues 1-45
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                                                                                                                                                                                                                                           ##cross-references EMBL:X66979; NID:g505486; PID:g505487
                                                                                                                                                                                                                                                                                        ##status
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             MDGTIKEALSVVSDDQSLFDSAYGASSHLSKADMTASANPDYGQPHKINPIPPQQDWINQ
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478
                                                                                              #domain ets RII regulatory region homology #label
#domain ets DNA-binding domain homology #label ET
#length 453 #molecular-weight 51015 #checksum 774
                                                                                                                                                                    #superfamily transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology
DNA binding; nucleus; proto-oncogene; transcription factor;
                                                                                                                                                                                                                                                                                                               Befort, J.J.; Remy, P.
Mech. Dev. (1993) 44:109-121
X1-f11, the Xenopus homologue of the f11-1
during embryogenesis in a restricted patt
neural crest cell distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transforming
Friend leuker
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                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Xenopus laevis #common_name African clawed
07-May-1995 #sequence_revision 23-May-1997 #text_change
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                                                                                                                                                       transforming protein
                                                                                                                                                                                                                                                          1-453 ##label MEY
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orming protein fli - African clawed frog
leukemia integration protein 1; transcription
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                                         Score 1740;
Pred. No. 0.(
91; Mismatc)
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       heavy-chain gene expression.
#cross-references MUID:94019387
#accession A54617
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                                   174
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##note sequence extracted from NCBI backbone (NCBIN:138523)
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##residnee
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                                                 DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGAAFIFPN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSYHSHQQKVNEVPSHPSSMPVTSSGFFGATSPYWNSPSANIYPNPNVPRHPNTHVQSHL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSRLANPGSGQIQLWQFLLELLSDSSNASCITWEGTNGEFKMTDPDEVARRWGERKSKPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAV-R---RSG--WGNSMSSP-VTKSPPM-G-GTQ-NVNK-S-GDQQRSQPDPYQILGPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TINERRVIVPADPALWSQDHVRQWLEWAIKEYGLVEIDCSLFQNIDGKELCKMSKEDFLR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ
TSVYPEATORITTRPDLPYEPPRRSAWTGHSHLTPQSKAAQPSPSAVPKTEDQRPQLDPY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQPHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNT---RLPAAHMPSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNYDKLSRALRYYYDKNIMTKYHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDFHGIAQA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNYDKLSRALRYYYDKSIMTKVHGKRYAYKFDFHGIAQALQPHPTDTSMYKYP-SEFSYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPN
                                                                                                h 45.3%;
Similarity 82.4%;
225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           A54617
A54617
Rivera, R.R.; Stuiver, M.H.; Steenbergen, R.; Murro, C
Mol. Cell. Biol. (1993) 13:7163-7169
Ets proteins: new factors that regulate immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A54617 #type fragment
transcription factor erg - mouse (fragment)
Ig heavy chain enhancer-binding protein
#formal_name Mus musculus #common_name house mouse
25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
30_May-1997
                                                                                                                                                                                                              #superfamily transcription factor erg; ets DNA-binding domain homology; ets RII regulatory region homology DNA binding; phosphoprotein; proto-oncogene; transcription factor; transforming protein
                                                                                                                                                               #domain ets DNA-binding domain homology #length 272 #checksum 3754
                                                                                                                                                                                                                                                                                                                                 1-272 ##label RIV
                                                                                                Score 1571; DB 2; I
Pred. No. 6.02e-302;
17; Mismatches 28;
                                                                                                                                Length
                                                                                                  Indels
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Best Local S
Matches 22
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52-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:M93255; NID:g18265; PID:g182661
##note the nucleotide sequence was submitted to
Library, May 1992
 257
                                 169
                                                                197
                                                                                                                             137
                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GDB:127565; OMIM:193067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
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                NSG-LNKS-PPLG-GAQ----TISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFL 221
                                                                                                                                                                                         SRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNMTTNERRVIVPADPTLWST 136
                                                                                                                                                                                                           ARESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNMTTNERRVIVPADATLVTQ 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESSL--LAYNTTSHT-DQSSRL-SVKE---D----P--S-Y-DSV-R----R-G-AWGNNM
|::| |::| |: : |:|| :: | | | | |: | | | |: |
                                                                                                                            DHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLR
                                                                                                                                                         EHVROWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGIAQALQPHAHPQKMNFVAPHPPALPVTSSSF
RSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFL
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                                                                                                                                                                                                                                                           229;
                                                                                                                                                                                                                                                                       40.48;
Similarity 56.48;
                                                                                                                                                                                                                                                                                                                                                                               #superfamily transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology
alternative splicing; DNA binding; nucleus; proto-oncogene;
transcription factor; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hromas, R.; May, W.; Denny, C.; Raskind, W. R.A.; Beck, E.; Klemsz, M.J.
Blochim. Biophys. Acta (1993) 1172:155-158
Human FLI-1 localizes to chromosome 11Q24 a transcript in neuroepithelioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $29844 #type complete transforming protein fli, short splice Friend leukemia integration protein 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Homo sapiens #common_name man 02-Dec-1993 #sequence_revision 23-May-1997 02-Sep-1997
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                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation
                                                                                                                                                                                                                                                        Score 1401; DB 1;
Pred. No. 5.17e-265;
69; Mismatches 73;
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                                                                                                                                                                                                                                                                                    Length 385;
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                             #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-173 ##label QIA
##cross-references GB:M81067; NID:g161310; PID:g161311
##cross-references GB:M81067; NID:g161310; PID:g161311
#superfamily transcription factor erg; ets DNA-binding homology; ets RII regulatory region homology
                                                                                                                                                                                                                                                                                 425
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##residues
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##molecule_type
             ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 SGQIQLWQFLLELLSDSSNANCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSR 60
                                                                                                                                                                                                                                                                                                                                                           ALRYYYDKNIMTKVHGKRYA-YKFDFAGLAQAMQPVQADPSMYRYQ-SDLT-YLPGY-HP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMPVTSSSFFGAASQYWTS-TGGIYPNPNVPRHPNTHVPSHLGSYY::|||||||:|:|||||:||
ALPVTSSSFFAAPNPYWNSPTGGIYPNT---RLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                TKLNFVGT-PIN-PSTNASLFSSHSSYWSSPTGANIYPSGHVTHPHASHMSSHIGTYY 172
                                                                                                                                                                                                                                                                                                                                                                                                     SGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSR 366
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                                                                                                                                                                                                                                                                                                                                          ALRYYYDKNIMTKVHPPESSMYKYP-SDLP-YMSSYHGKRYAYKFDFHGIAQALQPHAHP 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTKVHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQPHAHPQKMNFVAPHPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.5%;
Similarity 61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A56646
A56646
Qi, S.; Chen, Z.Q.; Papas, T
QiA Seq. (1992) 3:127-130
The sea urchin erg homolog d
erg-specific domain.
A56646
                                      Leprince, D.; Fontaine, F. FEBS Lett. (1994) 354:62-66 Identification of two ets related polychaete annelid Nereis divers
                                                                                                                                             diversicolor) (fragment)

#formal_name Nerels diversicolor #common_name sandworm
15-Jul-1995 #sequence_revision 23-May-1997 #text_change
30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Lytechinus variegatus #common_name variegated
                             S51226
                                                                                                                                                                                                      $51226 #type fragment
transcription factor erg/fli-1 homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain
#length 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA binding; nucleus; transcription factor
                                                                                                   Lelievre-Chotteau, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
preliminary
DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ets DNA-binding domain homology #checksum 5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 745; DB 2; L
Pred. No. 1.85e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                  Laudet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.S.; Lautenberger, J.A.
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                                           diversicolor
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                                                                                                     Flourens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-103 ##label CHE
##cross-references EMBL:M88475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GSGQIQLWQFLLELLSDSANSHIITWEGTNGEFKLVDPDETARRWGERKSKPNMNYDKLS
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Similarity 57.5%;
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Similarity 77.6%;
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homology; ets RII regulatory region homology
DNA binding; nucleus; transcription factor
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homology; cts RII regulatory region homology
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Isolation and characterization of five Drosophila encode an ets-related DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transforming protein cts-6
#formal_name Drosophila melanogaster
31-Dec-1993 #sequence_revision 31-Dec-1993
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transcription factor cts-21C -
melanogaster) (fragment)
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                                                                                                                                                                                                                                                                                                                          DNA binding; nucleus; transcription factor
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#type fragment
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Pred. No. 3.93e-113;
36; Mismatches 28;
                                                                                                                                                                                                  Score 519; DB 2; Le
Pred. No. 1.57e-77;
11; Mismatches 7;
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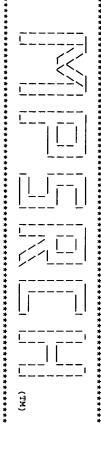
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#cross-references MUID:90384849
#accession S11224
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##cross references EMBL:X52691; NID:g64616; PID:g64617
IFICATION #superfamily transcription factor cts; ets DNA-bind1
homology; ets RII regulatory region homology
DNA binding; nucleus; phosphoprotein; transcription
 285
                                                                                                                                                                                                                                                                  ##molecule_type mRNA
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##cross-references EMBL:M88473
                               137 DRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPD 196
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FICATION #superfamily transcription factor crg; ets DNA-binding homology; ets RII regulatory region homology DS DNA binding; nucleus; transcription factor
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Local Similarity 93.8%; Pred. No. 5.79c-67;
hes 61; Conservative 4; Mismatches 0
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 QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPD
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                                                                    60;
                                                                                  13.2%;
Similarity 51.7%;
                                                                                                                                                                                                                                                                                                                                   N.; Remy, P.
Nucleic Acids Res. (1990) 18:5298
Characterization of Xenopus laevi
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sli224 #type fragment
transcription factor ets.1b - African clawed frog (fragment)
#formal_name Xenopus laevis #common_name African clawed frog
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
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S28819
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Stiegler, P.; Wolff, C.M.; Baltzinger, F.; Meyer, D.; Ghysdael,
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Dev. Biol. (1992) 151:176-191
Isolation and characterization of five Drosophila
encode an ets-related DNA binding domain.
                                                                                                                                   #domain ets DNA-binding domain #length 268 #checksum 3247
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No. 3.80e-65;
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Best Local Similarity 51.7%;
Matches 60; Conservative
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#accession S11225
   #journal
                                                                                                                             #accession
                                                                                                                                            #submission
                    #authors
                                            ##cross-reterences EMBL:X53953; NID:g50870;
##experimental_source strain BALB/C, thymus
                                                                     ##molecule_type mRNA
##residues 1-440 ##label GRA
##cross-references EMBL:X53953; N.
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                                                                                                                                                                                                                                                                                                                                                                                                    367 EVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKT-AGKRYVYRFVCDLQSLLGY 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 DRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-438 ##label STI 1-438 ##label STI 1-438 ##cross-references EMBL:X52692; NID:g64614; PID:g64615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345
                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##experimental_source oocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197
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                                                                                                                                                                                                                                                                                                                                                                                 EVARRWGERKSKPMMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY 400
                                                                                                                                                                                                                transcription factor ets-1, splice form a - mouse transcription factor p54; transforming protein ets-1a #formal_name Mus musculus #common_name house mouse 31-Mar-1992 #sequence_revision 23-May-1997 #text_change 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S11225
S11224
Stiegler, P.; Wolff, C.M.; Baltzinger,
Stiegler, P.; Wover, D.; Ghysdael, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily transcription factor ets; ets DNA-binding doma homology; ets RII regulatory region homology alternative splicing; DNA binding; nucleus; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ets-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factor p54; transforming protein ets-la
#formal_name Xenopus laevis #common_name African clawed
18-Feb-1994 #sequence_revision 23-May-1997 #text_change
23_May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #type complete transcription factor ets-l frog
Gunther, C.V.; Nye, J.A.; Bryner, Genes Dev. (1990) 4:667-679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain ets RII regulatory region homology #label ETS2\
#region helix-loop-helix #status predicted\
#domain ets DNA-binding domain homology #label ETS\
#region nuclear location signal
#length 438 #molecular-weight 50267 #checksum 6611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterization of Xenopus laevis cDNA clones
                                                                                                                           submitted to the EMBL Data A30487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res.
                                                                                                                                                                                                  A30487; A35875
                                                                                                                                                               Graves, B.J.
                                                                                                                                                                                A30487
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                                                                                                                                                                                                                                                                                                          #type complete
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Pred. No. 3.80e-65;
25; Mismatches 30
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                                                    thymus
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Stehelin,
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                  Graves,
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helin, D.; F
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FEATURE
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337-415
377-383
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57-130
97-130
337-415
377-383
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REFERENCE
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CLASSIFICATION
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ENTRY
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                                                       SUMMARY
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Matches
 Query Match
Best Local
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#title
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                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:94187072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 170-440 ##label
##cross-references EMBL:X53953
                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
##resider
                                                                                                                                                                                                                                                              ##residues 1-441 ##label
##cross-references GB:L20681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPD
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||||||| ||:||:|||:||||||||||| : ;|: ;| ; ;|
EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRADLNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 13.2%;
Similarity 51.7%;
60; Conservative
 Similarity
                                                                                                                                                                                                                                                                                                                                               J. Virol. (1994) 68:2320-2330

Effects of provirus integration in the Tpl-1/Ets-1 locus in Moloney murine leukemia virus-induced rat T-cell lymphomas: levels of expression, polyadenylation, transcriptional initiation, and differential splicing of the Ets-1 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #superfamily transcription factor ets; ets DNA
homology; ets RII regulatory region homology
alternative splicing; DNA binding; nucleus; ph
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9 15
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                                                    #length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A53988
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ellacosa, A.; Datta, K.; Bear, S.E.; Patriotis, P.A.; Copeland, N.G.; Jenkins, N.A.; Tsichlis, Virol. (1994) 68:2320-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0
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                                                  #domain ets RII regulatory region homology #label ETS2\
#region hellx-loop-hellx #status predicted\
#domain ets DNA-binding domain homology #label ETS\
#region nuclear location signal
#region nuclear location signal
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#region helix-loop-helix #status predicted\
#domain ets DNA-binding domain homology #label ETS\
#region nuclear location signal
#region nuclear location 50201 #checksum 2673
 13.2%;
51.7%;
Score 456; DB 1;
Pred. No. 9.60e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 456; DB 1;
Pred. No. 9.60e-65;
25; Mismatches 30
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NID:g404781; PID:g404782
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

in on: Wed Apr 7 09:44:50 1999; MasPar time 13.89 Seconds 923.482 Million cell updates/sec

bular output not generated.

Description: Perfect Score:

Sequence: >US-08-878-177-4
(1-478) from US08878177.pep
3467
1 MASTIKEALSVVSEDOSLFE.....IYPNTRLPAAHMPSHLGTYY 478

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 49.703; Variance 83.064; scale 0.598

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| No. | Score | Query Match | Length [| . B | ID | Description | Pred. No. |
|-----|-------|----------------|----------|------------|--------------|------------------------|-----------|
| 1 | 2608 | 75.2 | 462 | - 3 | ERG_HUMAN | TRANSFORMING PROTEIN E | 0.00e+00 |
| 2 | 1776 | 51.2 | 452 | ۳ | \mathbf{r} | NE (ERGB | 0.00e+00 |
| ω | 1773 | 51.1 | 452 | ۳ | FLI1_MOUSE | 뛵. | • |
| 4 | 1740 | 50.2 | 453 | H | | | |
| ر. | 1571 | 45.3 | 272 | - | ERG_MOUSE | z | |
| 6 | 745 | 21.5 | 173 | - | ERG_LYTVA | $\overline{}$ | 7.38e-144 |
| 7 | 519 | 15.0 | 102 | ۳ | ETS6_DROME | DNA-BINDING PROTEIN D- | 1.26e-89 |
| 8 | 459 | 13.2 | 64 | ۳ | ETS3_DROME | PROTEIN | 1.46e-75 |
| 9 | 458 | | 268 | ۳ | ET1B_XENLA | C-ETS-1B PROTEIN (XE1- | 2.49e-75 |
| 10 | 458 | 13.2 | 438 | 4سو | ET1A_XENLA | PROTEIN. | 2.49e-75 |
| 11 | 456 | | 440 | ۱., | ETS1_MOUSE | C-ETS-1 PROTEIN (P54). | 7.28e-75 |
| 12 | 456 | 13.2 | 441 | - | ETS1_RAT | -1 PROTEIN | √ |
| 13 | 456 | | 441 | ب | ETS1_HUMAN | C-ETS-1 PROTEIN (P54) | ~ |
| 14 | 453 | 13.1 | 472 | ۲ | ET2A_XENLA | C-ETS-2A PROTEIN. | 3.63e-74 |
| 15 | 452 | 13.0 | 441 | μ | ETSA_CHICK | TRANSFORMING PROTEIN P | 6.19e-74 |
| 16 | 452 | • | 454 | 1 | GABA_HUMAN | GA BINDING PROTEIN ALP | -7 |
| 17 | 452 | 13.0 | 454 | <u>س</u> و | GABA_MOUSE | PROTEIN | -7 |
| 18 | 452 | ٠ | 464 | μ | ELG_DROME | DNA-BINDING PROTEIN D- | |
| 19 | 450 | | 472 | μ | ET2B_XENLA | C-ETS-2B PROTEIN. | |
| 20 | 452 | 13.0 | 485 | μ | ETSB_CHICK | TRANSFORMING PROTEIN P | 6.19e-74 |
| 21 | 447 | • | 479 | ۳ | ETS2_CHICK | | |
| 22 | 448 | 12.9 | 669 | μ | MYBE_AVILE | P135-GAG-MYB-ETS TRANS | 5.26e-73 |
| 23 | 445 | 12.8 | 468 | μ | ETS2_MOUSE | C-ETS-2 PROTEIN. | 2.61e-72 |
| | | | | | | | |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | <u>ა</u> | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
|------------|------------------------|------------------------|-----------------------|-----------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------|
| 347 | 368 | 371 | 383 | 383 | 393 | 394 | 395 | 395 | 397 | 397 | 401 | 407 | 407 | 404 | 419 | 425 | 425 | 434 | 434 | 440 | 445 |
| 10.0 | 10.6 | 10.7 | 11.0 | 11.0 | 11.3 | 11.4 | 11.4 | 11.4 | 11.5 | 11.5 | 11.6 | 11.7 | 11.7 | 11.7 | 12.1 | 12.3 | 12.3 | 12.5 | 12.5 | 12.7 | 12.8 |
| 612 | 409 | 407 | 431 | 405 | 250 | 430 | 429 | 428 | 551 | 548 | 341 | 555 | 551 | 335 | 510 | 477 | 477 | 718 | 623 | 110 | 469 |
| _ | _ | H | Н | μ | Н | \vdash | _ | H | <u> </u> | Ц | _ | ᆫ | ᆫ | ٢ | _ | ш | _ | _ | | ju. | |
| ELF1_MOUSE | ELK3_MOUSE | ELK3_HUMAN | SAPA_HUMAN | SAPB_HUMAN | ETV3_HUMAN | SAPA_MOUSE | ELK1_MOUSE | ELK1_HUMAN | ERF_MOUSE | ERF_HUMAN | ETV2_HUMAN | ETV4_MOUSE | ETV4_HUMAN | ETV2_MOUSE | ERM_HUMAN | ETV1_MOUSE | ETV1_HUMAN | PNT2_DROME | PNT1_DROME | ETS2_LYTVA | ETS2_HUMAN |
| × | ETS-DOMAIN PROTEIN ELK | ETS-DOMAIN PROTEIN ELK | SERUM RESPONSE FACTOR | SERUM RESPONSE FACTOR | ETS-RELATED PROTEIN PE | SERUM RESPONSE FACTOR | ETS-DOMAIN PROTEIN ELK | ETS-DOMAIN PROTEIN ELK | ETS-DOMAIN TRANSCRIPTI | ETS-DOMAIN TRANSCRIPTI | ETS-RELATED PROTEIN 71 | POLYOMAVIRUS ENHANCER | ADENOVIRUS E1A ENHANCE | ETS-RELATED PROTEIN 71 | ETS-RELATED PROTEIN ER | ER81 PROTEIN (ETS TRAN | ETS TRANSLOCATION VARI | ETS-LIKE PROTEIN POINT | ETS-LIKE PROTEIN POINT | C-ETS-2 PROTEIN (FRAGM | C-ETS-2 PROTEIN. |
| 6.23e-50 | 1.17e-54 | 2.44e-55 | 4.62e-58 | 4.62e-58 | 2.43e-60 | 1.44e-60 | 8.50e-61 | | 2.97e-61 | 2.97e-61 | 3.61e-62 | 1.52e-63 | 1.52e-63 | 7.42e-63 | 2.66e-66 | 1.10e-67 | 1.10e-67 | 9.21e-70 | 9.21e-70 | 3.77e-71 | 2.61e-72 |

ALIGNMENTS

| KW DR | | ᄝᅲᄝ | Б В | 88 | 88 | 33 | Ŗ ₽ | 2 2 | j 5 | P.P. | RΑ | RX | R R | RL | RA | RX | RP | RN | R. | ₽: | R ? | RR | 8 | გ | SO | G E |) C | 3 5 | ď | Å | RESULT |
|---|--|-----|--|--------------|---|------------------------------------|---|--------------------|-----|------|--------|--------------------|----------------------------------|----------------------------|-----------------------------|-----------|-------------------------------|-----|----------|---------------|-------------------|---------------------|---|----------|-----------------------|------|------------------------|----------------|--------------|------|----------------------------------|
| PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PROSITE; PS50061; ETS_DOMAIN_3; 1. NUCLEAR PROTEIN; TRANSFORMING PROTEIN; DNA-BINDING; ALTERNATIVE INITIATION; PROTO-ONCOGENE; CHROMOSOMAL TRANSLOCATION. | TRANSFAC; T00265; TRANSFAC; T00266; MIM: 165080: - | •• | -:- SIMILARITY: BELONGS TO THE ETS FAMILY. EMBL; M17254; G182187; | ERG AND FUS. | DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML) IS CHAI | -1- SUBCELLULAR LOCATION: NUCLEAR. | ICHIKAWA H., SHIMIZU K., HAYASHI Y., OHKI M.; | MEDLINE; 94243799. | [4] | GE | GAG N. | MEDLINE; 94356859. | [3] CHROMOSOMAL TRANSLOCATION | C. NATL. ACAD. SCI. U.S.A. | S.P., RAO V.N., PAPAS T.S.; | 87317608. | SEQUENCE OF 100-462 FROM N.A. | [2] | 9(1987). | M E., REDDY P | MEDITUE: 87263429 | SECULATION EDON N 3 | | RYOTA; M | HOMO SAPIENS (HUMAN). | ERG. | (REC. 54, LAST ANNOTAL | (REL. 11, LAST | 11, CREATED) | 308; | ERG HUMAN STANDARD: PRT: 462 AA. |

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RESULT
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Best Local Similarity 82.7%;
Matches 396; Conservative
                                                  SEQUENCE FROM N.A.
MEDLINE; 93075640.
WATTSON D.K., SMYTH F
PAPAS T.S., SETH A.;
CELL GROWTH DIFFER.
                                                                                                                                                                                         Q01543;
01-JUL-1993 (REL.
01-JUL-1993 (REL.
01-NOV-1997 (REL.
                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUENBONE MARROW;

MEDLINE: 92396239.

DELATTRE O., ZUCMAN J., PLOUGASTEL
PETER M., KOVAR H., JOUBERT I., DE
NATURE 359:162-165(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
CHAIN
DNA_BIND
SEQUENCE
             SEQUENCE FROM N.A.
MEDLINE: 93007976.
PRASAD D.D., RAO V.N., REDDY E
CANCER RES. 52:5833-5837(1992)
                                                                                         NATURE
[2]
SEQUENCE
                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                  FLI-1 ONCOGENE
                                                                                                                                                                                                                        FLI1_HUMAN
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EL. 26, LAST SEQUENCE
EL. 35, LAST ANNOTATIO
(ERGB TRANSCRIPTION F
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462
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52031
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                                                  3:705-713(1992).
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                                                                  THOMPSON D.M.,
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Pred. No. 0.00e+00;
27; Mismatches 29
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ETS-DOMAIN.
                    E
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G P., ROULEAU
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Query Match
Best Local S
Matches 27
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EMBL; X67001; G32530; --
EMBL; M98833; G182189; --
EMBL; M98835; G182660; --
EMBL; M98255; G182660; --
PDB; 1FLI; 15-SEP-95.
TRANSFAC; T02066; --
MIM; 193067; --
PROSITE; PS00346; ETS_DOMAIN,
PROSITE; PS00346; ETS_DOMAIN,
PROSITE; PS00361; ETS_DOMAIN,
PROSITE; PS0061; ETS_DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTO-ONCOGENE; CDN_BIND 281
CONELICT 69
CONFLICT 17
CONFLICT 130
CONFLICT 323
CONFLICT 323
CONFLICT 323
CONFLICT 325
CONFLICT 426
SEQUENCE 452 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=BLOOD;
MEDLINE; 93176799.
HROMAS R., MAY W., D:
BECK E., KLEMSZ M.J.
BIOCHIM. BIOPHYS. AC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00345; PROSITE; PS00346; PROSITE; PS50061; PROSITE; PS50061; PRANSCRIPTION REGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95292091

LIANG H., MAO X., OLEJNICZAK E.T., NETTESHEIM D.G., YU L MEADOWS R.P., THOMPSON C.B., FESIK S.W.;

NAT. STRUCT. BIOL. 1:871-875(1994).

-!- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATO

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- SUBCELLULAR LOCATION TO THE DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED CHROMOSOMAL TRANSLOCATION T(11:22)(Q24:Q12) WHICH IN THE PROPERTY OF THE PROPERTY
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PSYHAHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHL
                                               MNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYP-SDISYM
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278; Conser
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larity 57.4%;
Conservative
                                                                                                                                                                                                                                                                                     R-G-AMGNNMNSG-LNKS-PPLG-GAQ----TISKNTEQRPQPDPYQILGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345; ETS_DOMAIN_1; 1.
346; ETS_DOMAIN_2; 1.
061; ETS_DOMAIN_3; 1.
REGULATION; ACTIVATOR;
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ACTA 1172:155-158(1993)
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391
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MISSING (IN REF. 4).

P -> A (IN REF. 4).

W -> V (IN REF. 4).

E -> O (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2 AND 4).

W; 192476F7 CRC32:
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Pred.
86; M
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d. No. 0.00e+
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Best Local S
Matches 27
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-!- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RE
THE DNA SEQUENCE 5'C[CA]GGAAQT-3'.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- TISSUE SPECIFICITY: EXPRESSED IN BOTH HEMATOPOIETIC AND
NONHEMATOPOIETIC TISSUES.

-!- INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLONES W
F-MULV INSERTIONS UP-STREAM OF THE FLI-1 LOCUS.

-!- DISEASE: INVOLVED IN ERYTHROLEUKEMIA INDUCTION BY FRIEND |
LEUKEMIA VIRUS (F-MULV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND SEQUENCE
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STRAIN-BALB/C; TISSUE-SPLEEN;
MEDLINE; 91257578.
BEN-DAVID Y., GIDDENS E.B., L
GENES DEV. 5:908-918(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLI1 OR FLI-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-MOV-1995 (REL. 32, LAST ANOOTATION UPDATE)
RETROVIRAL INTEGRATION SITE PROTEIN FLI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLI1_MOUSE P26323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; x59421; G50975; -. PIR; S17403; S17403.
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ZHANG L., LEMARCHANDEL V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:95554; FLI1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTO-ONCOGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFAC; T01408;
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                                                                                                                                                                                                                                                                                                                                     P-VRVNVKREYD--HMNGSRESPVDCSVSKCNKLVGGGEANPMNYNSYMDEKNGPPPPNM 117
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LTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYP
                                                                                                                                               TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR
                                                                                                                                                                                                                                                                                       PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM 118
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| Similarity 57.2%;
| 277; Conservative
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452 AA;
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51002 MW;
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Pred. No. 0.00e+00;
89; Mismatches 80
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Best Local S
Matches 27
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MEYER D., WOLFF C.M., STIEGLER P., SE
BEFORT J.J., REMY P.;
MECH. DEV. 44:109-121(1993).

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- DEVELOPMENTAL STAGE: EXPRESSED DU
-!- SIMILARITY: BELONGS TO THE ETS FE
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P41157;
01-FEB-1995 (REL. 31, CR
01-FEB-1995 (REL. 31, LA
01-FEB-1995 (REL. 31, LA
RETROVIRAL INTEGRATION S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND SEQUENCE
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PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
TRANSCRIPTION REGULATION; ACTIVATOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENOPUS LAEVIS (AFRICAN CLAWED EUKARYOTA; METAZOA; CHORDATA; 1
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                         EAV-R---RSG--WGNSMSSP-VTKSPPM-G-GTQ-NVNK-S-GDQQRSQPDPYQILGPT 270
                                                                                                                                                                                                    TINERRVIYPADPALWSQDHYRQWLEWAIKEYGLYEIDCSLFQNIDGKELCKMSKEDFLR 176
                                                                                                                                                                                                                                                                                       P-MRVNIKREYE--HMNGSRESPVDCSINKCSKLIGGSEGNAMTY-TYMDEKNGPPPPNM 116
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EATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPT
                                                                                       LTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYP
                                                                                                                                 STSIYNTEVLLSHLNYLRDSS-SSLGYNTQAHT-DQSSRLT-AKE---D----P--S-Y-
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273; Conser
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llarity 56.4%;
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Pred. No. 0.00e+00;
91; Mismatches 83
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Best Local S
Matches 22
ERG_LYTVA
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NON_TER
SEQUENCE
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PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
NUCLEAR PROTEIN; TRANSFORMING PROTEIN;
NUCLEAR PROTEIN; TRANSFORMING PROTEIN;
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-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- SIMILARITY: BELONGS TO THE ETS FAMILY.
EMBL; S66169; G436277; -.
MGD; MGI:95415; ERG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 94019387.
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANOTATION UPDATE)
TRANSFORMING PROTEIN ERG (FRAGMENT).
                                                                                                      412
                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475
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                                                                                                                                                                                                                                                                                                                      QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTYY
                                                                                                                                                                                                                                                                                                                                                                                                            TSVYPEATQRITTRPDLPYEPPRRSAWTGHSHLTPQSKAAQPSPSAVPKTEDQRPQLDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNYDKLSRALRYYYDKSIMTKVHGKRYAYKFDFHGIAQALQPHPTDTSMYKYP-SEFSYM
                                                                                                      HGIAQALQPHAHPQKMNFVAPHPPALPVTSSSF
                                                                                                                               RKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYP-
                                                                                                                                                                                                                                                                                           QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE
                                                                                                                                                                                                                                                                                                                                                                                        TSVYPEATQRITTRPDLPYEQARRSAWTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGAAFIFPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNYDKLSRALRYYYDKNIMTKVHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDFHGIAQA
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                                                                                                                                                                                                 RKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESS-MYKYPSDLPYMSSYHGKRYAYKFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 45.3%;
Similarity 82.4%;
225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478
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272
272 AA;
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         STANDARD;
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272
30907 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1571; DB 1;
Pred. No. 0.00e+00;
17; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETS-DOMAIN.
         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D2C258D9 CRC32;
         173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
                                                                                                                                                     272
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RESULTANCE OF THE PROPERTY OF 
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Best Local S
Matches 11
   Query Match
Best Local Similarity
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MEDLINE; 93091246.
QI S., CHEN Z.Q., PAPAS T.S., LAUTENI
DNA SEQ. 3:127-129(1992).
-i- SUBCELULAR LOCATION: NUCLEAR.
-i- SIMILARITY: BELONGS TO THE ETS F/
EMBL; M81067; G161311; -.
                                                                                           DNA-BINDING;
NON_TER
DNA_BIND
NON_TER
SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q01414;
01-FEB-1995
01-FEB-1995
01-FEB-1995
ERG PROTEIN
ERG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                               FLYBASE;
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92249640.
CHEN T., BUNTING M., KARIM F
DEV. BIOL. 151:176-191(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDAT
DNA-BINDING PROTEIN D-ETS-6 (FRAGMENT).
ETS21C OR ETS-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETS6_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 92249640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUECHINOIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR PROTEIN; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 21.5%;
Local Similarity 61.8%;
hes 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \vdash
                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
L; M88475; G157198; -.
; S28823; S28823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALRYYYDKNIMTKVHGKRYA-YKFDFAGLAQAMQPVQADPSMYRYQ-SDLT-YLPGY-HP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGQIQLWQFLLELLSDSSNANCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKLNFYGT-PIN-PSTNASLFSSHSSYWSSPTGANIYPSGHYTHPHASHMSSHIGTYY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGG-IYPNTRL--P-AAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALRYYYDKNIMTKVHPPESSMYKYP-SDLP-YMSSYHGKRYAYKFDFHGIAQALQPHAHP 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSR 366
                                                                                                                                                                                                                                               PS00345; ETS
PS00346; ETS
PS00346; ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1
173 AA;
                                                                                     102
102
                                                                                                                                                                                                         9gn0005660; Ets21C.;
300345; ETS_DOMAIN_1; ;
300346; ETS_DOMAIN_2; ;
350061; ETS_DOMAIN_3; ;
3; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAZOA; ARTHROPODA; INSECTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIEGATUS (SEA URCHIN). METAZOA; ECHINODERMATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REL. 31,
(REL. 31,
HOMOLOG (F
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                                                                                              102
11704
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19690 MW;
   15.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KARIM F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                      TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR
O THE ETS
                                                                                              MW;
Score 519; DB 1;
Pred. No. 1.26e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 745; DB 1; L
Pred. No. 7.38e-144;
30; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETS-DOMAIN
6039FEE1
                                                                                                                                                          ETS-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAUTENBERGER
                                                                                              E3670F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THUMMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UPDATE)
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                                                                                                 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋧
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                  Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
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                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S28820; S28820.
FLYBASE; FBonnon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETS3_DROME
P29774;
01-APR-1993
01-APR-1993
01-FEB-1995
                                                                                                                                                                                                                                                                                                              ET1B_XENLA
P18756;
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
NON_TER
SEQUENCE
                                                    TISSUE=OVARY;

MEDLINE; 90384849.

STIEGLER P., WOLFF C.M., BALTZINGER M.,

MEYER D., GHYSDAEL J., STEHELIN D., BEFF

NUCLEIC ACIDS RES. 18:5298-5298(1990).
                                                                                                                                                                                                                                                   01-NOV-1990 (REL.
01-NOV-1997 (REL.
C-ETS-1B PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 92249640.
CHEN T., BUNTING M., KARIM F
DEV. BIOL. 151:176-191(1992)
                    SEQUENCE FROM
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                          EUKARYOTA;
                                                                                                                                                                                                             XENOPUS LAEVIS (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLYBASE; FBgn0005658; Ets65A.

PROSITE; PS00345; ETS_DOMAIN_1;

PROSITE; PS00346; ETS_DOMAIN_2;

PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETS65A OR ETS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-BINDING
TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 GSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306
                                                                                                                                                                                                                                                                                                                                                                                                                                  366 RALR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RALR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GSGQIQLWQFLLELLSDSNNASCITWEGTNGEFKLTDPDEVARRWGERKSKPNMNYDKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  سو
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO L; M88473; G157194; -.
                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RALRYYYDKNIMTKVHGKRYA-YKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RALRYYDKNIMTKVHPPESSMYKY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
60; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MELANOGASTER (FRUIT FLY).
METAZOA; ARTHROPODA; INSECTA;
                                                                                                                                                                                              METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                                                                                                                                                                                                                        (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REL. 25, CREATED)
(REL. 25, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
PROTEIN D-ETS-3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
llarity 93.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR PROTEIN
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                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                   . 16, CREATED)
. 16, LAST SEQUENCE UI
. 35, LAST ANNOTATION
(XE1-B) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
7372 MW;
                                                                                                                                                                                              CHORDATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 459; DB 1;
Pred. No. 1.46e-75,
4; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THUMMEL
                                                                                                                                                                                                                                                                        ON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAMILY.
                                                                         M., HIRZLIN
BEFORT N., F
                                                                                                                                                                                                                                                                                                                                                     268
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                                                                                                                                                                                            TETRAPODA;
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                                                                             REMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                             SENAN
                                                                                                                                                                                          AMPHIBIA;
                                                                                             'FJ
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     Matches
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Best Local 9
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Best Local :
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P18755;
01-NOV-1990
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                            VARSPLIC DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-ETS-1A PROTEIN
ETS-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X52691; G64617; -. EMBL; X65166; G517230; -. PIR; S11224; S11224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SALVATI A.L., MORABITO S., MERENDINO X., CARNEVALI F. SUBMITTED (APR-1992) TO EMBL/GENBAK/DDBJ DATA BANKS.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- SUBLIARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                          SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XENOPUS LAEVIS
                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                     DNA-BINDING; NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIRST 203 AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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les 60; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; x52692; G64615;
S11225; S11225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKT-AGKRYVYRFVCDLQSLLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY 400
     Similarity
60; Conser
                                                                                                                                                                                                                                                                                                                                                ; T02040; -. PS00345; ETS_DOMAIN_1; 1. PS00346; ETS_DOMAIN_2; 1. PS50061; ETS_DOMAIN_3; 1. PS500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00345; ETS_DOMAIN_1; 1.
PS00346; ETS_DOMAIN_2; 1.
PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90384849
                                                                                                        204
438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 16,
) (REL. 16,
) (REL. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
                                                                                                                                                                                                                                                332
153
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109
                                                                                                                                                                                                279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AFRICAN CLAWED FROG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%;
51.7%;
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109
                            13.2%;
51.7%;
                                                                                                                                                                                                                                                203
412
153
                                                                                                                                                                                                279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30772
                                                                                                                 50267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
Score 458; DB 1; Le Pred. No. 2.49e-75; 25; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 458; DB 1;
Pred. No. 2.49e-75;
25; Mismatches 3(
                                                                                                                                                                                                                   ; ALTERNATIVE SPLICING; PHOSPHORYLATION. MISSING (IN C-ETS-1A'). ETS-DOMAIN. PHOSPHORYLATION (BY CAM-KINASE) (POTENTIAL).
                                                                                                                                                        PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY (POTENTIAL). 6EF0772C CRC32;
                                                                                                                                          98.98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETS-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETS
                                                                                                              2CF39438
                                                                                                              IDENTITY TO C-ETS-1B PROTEIN 39438 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
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                                                                                                                                                                                          (BY CAM-KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N J.,
                                                     Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAM-KINASE)
  Indels
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P.;
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307 DRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPD 366

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285

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-I- SIMILARITY: BELONGS TO THE ETS FAMILY.

EMBL; M58482; G193192; -.

EMBL; X53953; G50871; -.

EMBL; X53953; G50871; -.

EMBL; X53953; G50871; -.

EMBL; X53967; A30487.

PIR: A30487; A30487.

PROB: 1ETC; 29-JAN-96.

TRANSFAC; TOO111; 1.

PROS: PS00346; ETS_DOMAIN_1: 1.

PROS: PS00346; ETS_DOMAIN_3: 1.

PROS: PS00346; ETS_DOMAIN_3: 1.

PROS: PS00346; ETS_DOMAIN_3: 1.

PROS: PS00346; ETS_DOMAIN_3: 1.

PROTO-ONCOGENE: DNA-BINDING; NUCLEAR PROTEIN; ALL PROSPHORYLATION; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETS1_MOUSE STAN
P27577; O61403;
O1-AUG-1992 (REL. 2
O1-FEB-1995 (REL. 3
15-JUL-1998 (REL. 3
    DNA_BIND
CONFLICT
CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN~BALB/C; TISSUE~THYMUS;
MEDLINE; 90370376.
CHEN J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. WATSON D.K., SETH A., (IN) ONCOGENESIS, PAPP COMPANY, HOUSTON, (19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-ETS-1 PROTEIN (P54).
ETS1 OR ETS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DONALDSON L.W., PETERSEN J.M., GRAVES EMBO J. 15:125-134(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96176767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 332-415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONCOGENE RES. 5:277-285(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPAS T.S., (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23, CREATED)
31, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
      ETS-DOMAIN.

D -> E (IN REF. 3).

L -> S (IN REF. 3).

AT -> SY (IN REF. 3).

G -> P (IN REF. 3).

L -> R (IN REF. 3).

E -> D (IN REF. 3).

E -> D (IN REF. 3).

C -> V (IN REF. 3).

D -> V (IN REF. 3).

D -> V (IN REF. 3).

D -> R (IN REF. 3).

D -> R (IN REF. 3).

A -> R (IN REF. 3).

C -> R (IN REF. 3).

C -> R (IN REF. 3).

A -> R (IN REF. 3).

C -> R (IN REF. 3).

C -> R (IN REF. 3).

C -> R (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHWEINFEST C.W., F
, PP. 221-232, GULF
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                                                                                                                                                                                                                                                                                                                                                          SPLICING;
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RESULT
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETS1_RAT STANDARD; PRT; 441
P41156;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDA
01-OCT-1996 (REL. 34, LAST ANNOTATION UP
C-ETS-1 PROTEIN (P54).
ETS1 OR ETS-1.
ETS1 OR ETS-1.
RATTUS NORVEGICUS (RAT).
EUKARYCTA; METAZOA; CHORDATA; VERTEBRATA
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE; 94187072.

BELLACOSA A., DATTA K., BEAR S.E., PATR.
COPPLAND N.G., JENKINS N.A., TSICHLIS P
J. VIROL. 68:2320-2330(1994).

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- SUBCELLULAR ITY: BELONGS TO THE ETS FAMI.

-!- SIMILARITY: BELONGS TO THE ETS FAMI.

EMBL; L20681; 6404782; -.

PIR; A53988; A53988.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS00361; ETS_DOMAIN_3; 1.

PROSPLATION.

DRACEPHORYLATION.
                                                                                                                       ETS1_HUMAN
P14921;
01-APR-1990
01-APR-1990
15-JUL-1998
C-ETS-1 PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND SEQUENCE
  SEQUENCE;
                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION.
DNA_BIND 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345
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                                                                                                                                                                                                                                                                                                                                                                                                           EVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKT-AGKRYVYRFVCDLQSLLGY
|||||| || :||:||:||:|||:|||:||:|::
EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY
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60; Conser
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Similarity 51.7%;
60; Conservative
FROM N.A.
89083219.
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413
440
                                                                                                                                        ) (REL. 14, C
) (REL. 14, I
8 (REL. 36, I
) OTEIN (P54)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 AA;
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larity 51.7%;
Conservative
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50423 MW;
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413
50201
                                                                              CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                        , CREATED)
, LAST SEQUENCE UPI
, LAST ANNOTATION (
, LAST ANNOTATION (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A., TSICHLIS P.N.;
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Pred. No. 7.28e-75;
25; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 456; DB 1;
Pred. No. 7.28e-75,
25; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETS-DOMAIN.
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R -> A (IN REF. 3)
18E90F01 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY.
                                                                                                                                        ON UPDATE)
CON UPDATE)
C-ETS-1B)
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Best Local
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                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 92158632.
BURDETT L.A., QI S.M., (
NUCLEIC ACIDS RES. 20:3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ET2A_XENLA
P19102;
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 8904ZUDO.
MEDLINE; 8904ZUDO.
WATSON D.K., MCWILLIAMS M.J.,
SCHWEINFEST C.W., PAPAS T.S.;
SCHWEINFEST ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                         ETS2A OR ETS-2A.
XENOPUS LAEVIS (AFRICAN CLAWED
EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- PTM: ISOFORMS OF ETS-1 ARE ALSO GENERATED BY DIFFERENTIAL
-!- PHOSPHORYLATION.
-!- DISEASE: ETS IS RESPONSIBLE FOR ERYTHROBLAST AND FIBROBLAST
TRANSFORMATION. THE JUXTAPOSITION OF THE INTERFERON AND C-ETS-1
PROTO-ONCOGENE MAY BE INVOLVED IN THE PATHOGENESIS OF HUMAN
MONOCYTIC LEUKEMIA.
-!- ALTERNATIVE PRODUCTS: ISOFORMS OF ETS-1 CAN BE GENERATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WERNER M.H., CLORE G.M., FISHER SHILOACH J., GRONENBORN A.M.; CELL 83:761-771(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REDDY E.S
ONCOGENE
                                                                                                                                                                                                                                                                                                                                                           C-ETS-2A PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1993
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN;
PROSPHORYLATION; 3D-STRUCTURE; ETS_DOMAIN
2016; PROSPHORYLATION; 3D-STRUCTURE; ETS_DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; 2STT; 12-MAR-97.
PDB; 2STW; 12-MAR-97.
TRANSFAC; T00112; -.
   SEQUENCE OF 121-472 FROM TISSUE-OCCYTE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 320-415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKT-AGKRYYYRFVCDLQSLLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96097120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244
441 AA;
                                                                                                                                                                                                                                                                                                                                                                                      (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%;
larity 51.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAO V.N.;
3:239-246(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      16, CREATED)
27, LAST SEQUENCE 36, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 N
50408 MW;
                                                                                              , CHEN Z.Q., LA :371-371(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 456; DB 1; Leny
Pred. No. 7.28e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETS-DOMAIN.
MISSING (IN C-ETS-1B).
; 958AFA4A CRC32;
                                                                                                                                                                                                                                                      ) FROG).
VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85:7862-7866(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAPIS P., LAUTENBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETS
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                                                                                                                                   LAUTENBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          À
                                                                                                                                                                                                                                                             TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING;
                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 441;
                                                                                                                                .
A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRINH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                             AMPHIBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Best I
                                                                       SEQUENCE FROM N.A.
MEDLINE: 89045631.
WATSON D.K., MCWILLIAMS M.J.
VIROLOGY 167:1-7(1988).
'I- FUNCTION: THIS PROTEIN I
ETS. IN THE E26 VIRUS, E
TRANSFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 90356411.
WOLFF C.M., STIEGLER E
STEHELIN D., BEFORT N.
NUCLEIC ACIDS RES. 18
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETSA_CHICK
P13474;
01-JAN-1990
01-JAN-1990
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                              GHYSDAEL
ONCOGENE
                                                                                                                                                                                                                                                                                                                                                                            TISSUE-SPLEEN;
TISSUE-SPLEEN;
MEDLINE; 88289026.
DUTERQUE-COQUILLAUD M., LEPRINCE D
DUTERQUE-COQUILLAUD M., STEHELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T02041; -.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

DNA-BINDING; NUCLEAR PROTEIN.

AAAC

ETS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLUS GALLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M81683; G214130; -
EMBL; X51826; G64619; -.
PIR; S10994; S10994.
PIR; S28824; S28824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEHELIN D., BEFORT N., REMY P.;
CELL GROWTH DIFFER. 2:447-456(1991).
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                        ONCOGENE
                                                                                                                                                                                                                                                             CHEN J
                                                                                                                                                                                                                                                                                                     TISSUE-SPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALLIFORMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOLFF C.M., STIEGLER STEHELIN D., BEFORT N
                                                                                                                                                                                                                                                                                MEDLINE; 88289029
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 KMNYEKLSRGLRYYYDKNIIHKT-SGKRYYYRFVCDLHNLLGY 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 ASILAGFTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLTDPDEVARRWGKRKNKP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                TISSUE SPECIFICITY: THYMUS. ALTERNATIVE PRODUCTS: ALTER C-ETS-1 GENE GENERATES TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSRLAN-PGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity
61; Conser
                                                                                                                                                                                                                                                                                                                                                              RES.
                                                                                                                                                                                                                                        RES.
                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF 121-472 FROM N.A. 92088972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 13, CREATED)
(REL. 13, LAST SEQUENCE UI
(REL. 31, LAST ANNOTATION)
PROTEIN P54/C-ETS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.1%;
llarity 59.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                              DEBUIRE B., STEH . 2:335-344(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RES. 18:4603-4604(1990)
                                                                                                                                                                                                                                        2:371-384(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
GENERATES
54 AND P68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ъ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ъ
;
                                                                                                                                                         M.J., PAPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REMY P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BALTZINGER M.,
                                   ALTERNATIVE
                                                                                              ETS 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 453; DB 1; Le
Pred. No. 3.63e-74;
16; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETS-DOMAIN.
; 064D44EA CRC32;
                                                                                              SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                  RNATIVE SPLICING PROTEINS HAVING
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D
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..
                                                                                            NORMAL CELLULAR RESPONSIBLE FOR
                                                                                                                                                           н
                                                                                                                                                                                                                                                                                                                                                                                                     FLOURENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.
                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ü,
              MECHANISM WITHIN THE DISTINCT N-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400
                                                                                              PRODUCT OF CHICKEN ERYTHROBLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHYSDAEL
                                                                                                                                                                                                                                                                                                                                                                                                       HENRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHYSDAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVES; NEOGNATHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
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CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.

DR EMBL; X12462; G211753; -.

DR EMBL; X13026; G63180; -.

DR EMBL; X13027; G63383; -.

DR PIR; X31285; TYCHTE.

DR PIR; S29132; S07625.

DR PIR; S29133; S29132.

DR TRANSFAC; T00114; -.

DR PROSITE; PS00346; ETS_DOMAIN_1; 1.

DR PROSITE; PS00346; ETS_DOMAIN_2; 1.

DR PROSITE; PS00346; ETS_DOMAIN_3; 1.

DR PROSITE; PS00346; ETS_DOMAIN_3; 1.

PROSITE; PS00346; ETS_DOMAIN_3; 1.

PROSITE; PS00346; ETS_DOMAIN_1; 1.

DR PROSITE; PS00346; ETS_DOMAIN_1; 1.

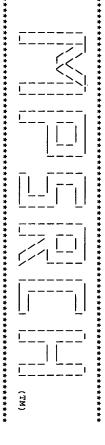
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PROSITE; PS00346; ETS_DOMAIN_2; 1.

DR PROSITE; PS00346; ETS_DOMAIN_2; 1.

ETS-DOMAIN.

ETS
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 7 09:32:06 1999; MasPar time 19.45 Seconds 868.394 Million cell updates/sec

ibular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-878-177-2 (1-451) from US08878177.pep 3286

1 MASTIKEALSVVSEDQSLFE.....IYPNTRLPAAHMPSHLGTYY 451

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Mean 48.029; Variance 92.580; scale 0.519

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 485 14.8 718 1 S33168 pointed protein, spin 483 14.7 468 1 TVMSE2 transcription factor 483 14.7 469 1 TVMSE2 transcription factor 484 14.7 472 1 A53326 transcription factor 482 14.7 488 1 TVFVES transcription factor 482 14.7 488 1 TVFVES transcription factor 482 14.7 488 2 TVFVES transcription factor 482 14.1 44 110 2 A45938 transcription factor 483 13.5 448 2 S28820 transcription factor 482 14.1 440 2 I48291 transcription factor 482 14.1 440 2 I48291 transcription factor 483 13.5 428 1 TVHUEK transcription factor 483 13.5 462 1 S35534 addenovirus ElA enhanc 431 13.5 462 1 TVHUEK transcription factor 437 13.3 428 1 TVHUEK transcription factor 437 13.3 428 1 TVHUEK transcription factor 438 13.5 462 1 S35534 addenovirus ElA enhanc 431 13.1 430 2 I48755 mSAPla - mouse 422 12.8 407 2 I38062 Net - human | 4 5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | |
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| protein, protein, protein, protein, protein, protein fa iption fa | I38062 | I48755 | JC4965 | TVHUEK | S24061 | S35534 | A46396 | S43692 | A54308 | B46396 | I38893 | 148291 | S28820 | S59133 | A45938 | TVCHE2 | TVFVES | A53236 | TVHUE2 | TVMSE2 | S33168 | CULTER |
| | Net - human | mSAPla - mouse | elk1 protein - mouse | transforming protein | transcription factor | adenovirus ElA enhanc | ets-related protein 7 | | l protein - | | | | transcription factor | | | | | | | fac | protein, | Process, |

ALIGNMENTS

| Qy 121 NERRVI | Db 121 NERRVI | Ob 61 PARVTI Qy 61 PARVTI | بر بر ا | Query Match Best Local Similarity Matches 451; Conse | 119-193 312-390 SUMMARY | KEYWORDS | #gene CLASSIFICATION | ##CIOSS TETETERCES | ##residues | ##status ##molecule_type | #accession | #cross-references | | #title | #journal | #authors | REFERENCE | | ORGANISM DATE | TITLE | RESULT 1 |
|--|--|---|---------|--|--|--|--|---|-----------------------------|-----------------------------|------------|--------------------|-----------------------|---------------------------|--|--|-----------|-------------|------------------|------------------------------------|-----------------------|
| NERRVIVPADPTLMSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT 180 | NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT 180 | PARYTIKMECNPNQVNGSRNSPDDCSVAKGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 | | h 91.0%; Score 2989; DB 1; Length 478; Similarity 94.4%; Pred. No. 0.00e+00; 451; Conservative 0; Mismatches 0; Indels 27; Gaps 2; | #domain ets RII regulatory region homology #label ETS2\ #domain ets DNA-binding domain homology #label ETS #length 478 #molecular-weight 53913 #checksum 547 | homoLogy; ets RII regulatory region homoLogy DNA binding; phosphoprotein; proto-oncogene; transcription factor; transforming protein | erg superfamily transcription factor erg; ets DNA-binding domain | telences Embh: A//139; NID:9/90439; FID:9/90440 | TWD: .Y77150: NTD: ~700430: | preliminary _type mRNA | \$60754 | nces MUID:95329425 | condensation and cart | expression of the chicken | Duterque-Coquillaud, M. Mech. Dev. (1995) 50:17-28 | Dhordain, P.; Dewitte, F.; Desbiens, X.; Stehelin, D.; | S60754 | 10-Jul-1998 | Š | transcription factor erg - chicken | S60754 #type complete |

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ORGANISM
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##molecule_type mRNA
##molecule_type mRNA
##residues 1-231,256-486 ##label REA
##coss-references GB:M17254; NID:g182186;
##CTOSS-references GB:M17254; NID:g182186;
##CTOSS-REFERENCE A94178
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#title Differentially spliced erg-3 product functions
transcriptional activator.
#cross-references MUID:94119611
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#cross-references MUID:87317608
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##molecule_type mRNA
##residues 230-259 ##label RES
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##cross-references GB:M21535; NID:g182182; #
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transforming protein erg-3 - human
transforming protein erg-1; transforming protein erg-2
#formal_name Homo sapiens #common_name man
31-Mar-1989 #sequence_revision 30-May-1997 #text_change
31-Oct-1997
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##molecule_type mRNA
1-68, 'V',70-129,'A',131-132,'V',134-322,'Q',324-425,
##residues 427-452 ##label HRO1
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l Similarity 89.3%;
427; Conservative
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T.; Peter, M.; Kovar, H.; Joubert, I.; de Jong,
Rouleau, G.; Aurias, A.; Thomas, G.
Nature (1992) 3599:162-165
Gene fusion with an ETS DNA-binding domain caused chromosome translocation in human tumours.
                                                                                   Hromas, R.; May, W.; Denny, C.; Raskind, W.; R.A.; Beck, E.; Klemsz, M.J.
Biochim. Biophys. Acta (1993) 1172:155-158
Human FLI-1 localizes to chromosome 11024 and transcript in neuroepithelioma.
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Pred. No. 0.00e+00;
20; Mismatches 3
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#title The human homolog of the mouse common viral region, FLII, maps to 11q23-q24.

#cross-references MUID:92112219

#accession 154170
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#accession A49015
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ap_position 11q24.1-11q24.3
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1-6 ##label RE2
~m.r.47616; NID:gl000863;
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##cross-references GB:S45205; NID:g257353; PID:g257354
##note sequence extracted from NCBI backbone (NCBIN:115336
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71.5%;
l Similarity 67.0%;
306; Conservative
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The ERGB/F11-1 gene: isolation and characterization of a number of the family of human ETS transcription factors.
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                                                                                                                                                                                          #superfamily transcription factor erg; ets DNA-binding doma homology; ets RII regulatory region homology alternative splicing; DNA binding; nucleus; proto-oncogene;
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Prasad, D.D.; Rao, V.N.; Reddy, E.S.
Cancer Res. (1992) 52:5833-5837
Structure and expression of human Fl
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Score 2348; DB 1; 1
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85; Mismatches 55;
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#accession $17403
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#residues 1-452 ##label
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                                                                      MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQPHKINPLPPQQEWINQ 60
                                                   MASTIKEALSVVSEDQSLFECAYGSP-HLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TINERRVIVPADPILMTQEHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-VRVNVKREYD--HMNGSRESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-VRVNVKREYD--HMNGSRESPVDCSVSKCNKLVGGGEANPMNYNSYMDEKNGPPPPNM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR 355
                                                                                                                                      11.2%;
Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ben-David, Y.; Giddens, E.B.; Letwin, K.; Bernstein, A. Genes Dev. (1991) 5:908-918
Erythroleukemia induction by Friend murine leukemia virus:
insertional activation of a new member of the ets gene family, Fli-1, closely linked to c-ets-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $17403 #type complete
transforming protein fli - r
Friend leukemia integration
                                                                                                                                                                                    #domain ets RII regulatory region homology #label
#domain ets DNA-binding domain homology #label ET
#length 452 #molecular-weight 51002 #checksum 8905
                                                                                                                                                                                                                                                        DNA binding; nucleus; proto-oncogene; transcription factor; transforming protein
                                                                                                                                                                                                                                                                                         #superfamily transcription factor erg; ets DNA-binding homology; ets RII regulatory region homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Mus musculus #common_name house mouse
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_c
                                                                                                                        Conservative
                                                                                                                    Score 2339; DB 1;
Pred. No. 0.00e+00;
85; Mismatches 56
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NID:g50974; PID:g50975
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ion protein
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 117
                                                                                                                                                                                                                                                                                                                                                                                        ##moleculc_type mRNA
##residues 1-453 ##label
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                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-453 ##label MEY
##cross-references EMBL:X66979; NID:g505486; PID:g505487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-MRVNIKREYE--HMNGSRESPVDCSINKCSKLIGGSEGNAMTY-TYMDEKNGPPPPNM
                                                                                          MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ
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TTNERRVIVPADPALWSQDHVRQWLEWAIKEYGLVEIDCSLFQNIDGKELCKMSKEDFLR
                              PPARVTIKMECNPNOVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPARVT I KMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH - I PPPNM
                                                                                                                                                     h 70.1%;
Similarity 65.9%;
302; Conservative
                                                                                                                                                                                                                                                                                           *superfamily transcription factor erg;
homology; ets RII regulatory region bnA binding; nucleus; proto-oncogene; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meyer, D.; Wolff, C.M.; Stiegler, P.; Senan, F.; Befort, Befort, J.J.; Remy, P. Mech. Dev. (1993) 44:109-121
X1-f11, the Xenopus homologue of the f11-1 gene, is expreduring embryogenesis in a restricted pattern evocative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $49013 #type complete transforming protein fli - African clawed frog Friend loukemia integration protein 1; transcr
                                                                                                                                                                                                               #domain ets RII regulatory region homology #label
#domain ets DNA-binding domain homology #label ET:
#length 453 #molecular-weight 51015 #checksum 774
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07-May-1995 #sequence_revision 23-May-1997 #text_change
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                                                                                                                                                                                                                                                                             transforming protein
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                                                                                                                                                     Score 2305; DB 1; Length 453; Pred. No. 0.00e+00; B5; M1smatches 59; Indels 1
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vocative of
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Best Local :
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217-295
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                                                                                                                                                                                                                                                                                                                                                  ##cross-references GDB:127565; OMIM:193067
ap_position llq24.1-11q24.3
                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:M93255; NID:g18265;
##note the nucleotide sequence was
Library, May 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
                                                             70
                                                                                           78 SRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNMTTNERRVIVPADPTLWST 136
                                                                                                             10 ARESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNMTTNERRVIVPADATLVTQ 69
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                               DHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLR
                                              EHVRQWLEWAIKEYSLMEIDTSFFQNWDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLR 129
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                                                                                                                                                                         60.0%;
Similarity 67.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hromas, R.; May, W.; Denny, C.; Raskind, W. R.A.; Beck, E.; Klemsz, M.J.
Blochim, Blochys. Acta (1993) 1172:155-158
Human FLI-1 localizes to chromosome 11024 (
transcript in neuroepithelioma.
                                                                                                                                                                                                                                                                                   #superfamily transcription factor erg; cts DNA-binding homology; cts RII regulatory region homology alternative splicing; DNA binding; nucleus; proto-oncog transcription factor; transforming protoin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S2984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $29844 #type complete transforming protein fil, short splice Friend leukemia integration protein 1;
                                                                                                                                                                                                                    #domain ets RII regulatory region homology #label #domain ets DNA-binding domain homology #label ET' #length 385 #molecular-weight 43437 #checksum 4889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Homo sapiens #common_name man 02-Dec-1993 #sequence_revision 23-May-1997 02-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                   GDB:FLI1
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-385 ##label HRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation not shown
                                                                                                                                                      Score 1973; DB 1;
Pred. No. 0.00e+00;
68; Mismatches 46
                                                                                                                                                          46;
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submitted t
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##note sequence extracted from NC
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                                                                                                                                                                                                                                                                 53 GAAFIFPNTSVYPEATQRITTRPDLPYEPPRRSAWTGHSHLTPQSKAAQPSPSAVPKTED 112
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                                                                                                                                                                                                         QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPD 172
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                                                                                                                                               EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPE 232
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                                                                        SSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSF
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Similarity 94.5%;
208; Conservative
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transcription factor erg - mouse (fragment)
Ig heavy chain enhancer-binding protein
#formal_name Mus musculus #common_name house mouse
25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily transcription factor erg; ets DNA-binding domain homology; ets RII regulatory region homology DNA binding; phosphoprotein; proto-oncogene; transcription factor; transforming protein
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A54617
   A56646 #ty
transcription
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#type fragment
on factor erg/fli-1 homolog
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3.79e-296;
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   sea urchin
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CLASSIFICATION #superfar
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Best Local Similarity 73.3%;
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##cross references GB:M81067; NID:g161310; PID:g161311
##CONTION #superfamily transcription factor erg; ets DNA
homology; ets RII regulatory region homology
DNA binding; nucleus; transcription factor
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ALRYYYDKNIMTKVHGKRYAYKFDFAGLAQAMQPVQADPSMYRYQSDLTYLPGYH--PTK 118
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A56646
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homology; ets RII regulatory region homology
DNA binding; nucleus; transcription factor
                                                                                                                                                                                                                                                                              Lelievre-Chotteau, A.; Laudet, V.; Flourens
Leprince, D.; Fontaine, F.
FEBS Lett. (1994) 354:62-66
Identification of two ets related genes in
                                                                                                                                                                                                                                                                                                                                                                      diversicolor) (fragment)

#formal_name Nereis diversicolor #common_name sandworm
15-Jul-1995 #sequence_revision 23-May-1997 #text_change
30-May-1997
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#formal_name Lytechinus variegatus #common_name variegated
                                                                                                                  #domain ets DNA-binding domain #length 179 #checksum 4104
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transcription factor erg/fli-1
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#length 173
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The sea urchin erg homolog erg-specific domain.
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                                                           Conservative
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                                                          Score
Pred.
32; M
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Pred. No. 6.95e-171;
27; Mismatches 12;
                                                           Mismatches
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                                                                       895; DB 2; L
No. 3.51e-157;
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##cross-references FlyBase:FBgn0004510
ntrons 22/1; 60/2; 83/3; 322/1
IFICATION #superfamily transcription factor elg; ets DNA-binding homology; ets RII regulatory region homology
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298-449 ##label CHE

##cross-references EMBL:M88471; NID:g157189; PID:g552088

##cross-references translated the codon AGC for

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##residues 1-4
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                                     -PRDPGNIFWTHLQLLKE--CNFV-SVVHKRAEE-QRKPKQPRIMSANSISTN-SGGSLS
                                                                                                                                                                                                                                                           NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDF-QRL 179
                                                                                                                                                                                                                                                                              EQIRLKIPEAANEWTHAHVTYWLEWAVKQFELVGINMSDWQ-MNGQELCAMTHEEFNQKL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQ 398
                                                                                                             TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTS-SRLANPGSGQIQLWQFLLELLSDSSN
                                                                                                                                                                                     TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RALRYYYDKNIMTKVHGKRYAYKFDFAGLAQAMQPSTTDPAAYKYQQDL-LMSGYH-HTS
                                                                                                                                                 LEQRIMRKSYQSV-KSSD-SVE-STTSSMNPSNYTTIGSGNNGQVQLWQFLLEILTDCEH
                                                                                                                                                                                                                                                                                                                                h 20.1%;
Similarity 39.6%;
97; Conscrvative
     426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S. Dev. Biol. (1992) 151:176-191
Isolation and characterization of five Drosophila encode an ets-related DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S37616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schulz, R.A.
Oncogene (1992) 7:2471-2478
Molecular characterization and structural organization of Drclg, an ets proto-oncogene-related gene of Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $37616; $28822
$37616
The, S.M.; Xie, X.; Smyth, F.;
                                                                                                                                                                                                                                                                                                                                                                                                       #domain ets RII regulatory region homology #label | #domain ets DNA-binding domain homology #label ETS #length 464 #molecular-weight 52658 #checksum 2714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Drosophila melanogaster
13-Jan-1995 #sequence_revision 23-May-1997
18-Sep-1998
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                                                                                                                                                                                                                                                                                                                              Score 660; DB 1; Length 464; Pred. No. 2.17e-107; 62; Mismatches 74; Indels
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ENTRY
TITLE
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Best Local
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322-400
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#cross-references MUID:91343912
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                                                                                                                                                                                                                                                                                                                                                                                                             176 EQERLGIPYDPIRWSTDQVLHWVVWVMKEFSMTDIDLTTL-NISGRELCSLNQEDFFQRV 234
                                                                                            360
                                                                                                                                397 YKF 399
                                                                                                                                                                  300 NCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYA
                                                                                                                                                                                                        337
                                                                                                                                                                                                                                          240 TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNS
                                                                                                                                                                                                                                                                              282
                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                       235 -PR--GEIIWSHLELLR-K----YVLASQE--QQMNE-IVTI-DQP-VQIIPAS-VPPATP 281
                                                                                                                                                                                                                                                                                                                                                                                      121 NERRYIVPADPTLMSTDHYRQWLEWAYKEYGLPDVDILLFQNIDGKELCKMTKDDF-QRL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA; protein
#*residues 1-454 ##label LAM
##resors-references GB:M74515; NID:9193382; PID:9193383
##arote parts of this sequence were detormined
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                                       12
                                                                                          YKF
                                                                                                                                                                                                    DCISWVGDEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDGDMICKVQGKRFV 396
                                                                                                                                                                                                                                                                                                                  TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP
                                                                                                                                                                                                                                                             TTIKVIN-SSAKAAKVQ-RSPRISGEDRSSP-GNRTGN--NGQIQLWQFLLELLTDKDAR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                              101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 19.9%;
Similarity 41.6%;
101; Conservative
                                                                                            362
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16 47.0
GA-binding protein is a heterotetramor beta-type chains.

(via
A48146
GA-binding |
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McKnight, S.L.
Science (1991) 253:789-792
Identification of ets- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A40858 #type complete
GA-binding protein alpha chain - mouso
GABBA; nuclear respiratory factor 2 alpha
transcription factor E4TF1 60K chain
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A40858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrom c oxidase chain IV, ATPase bota chain, and adenovirus E4 genes superfamily transcription factor elg; ets DNA-binding domain homology; ets RII regulatory region homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a transcription factor that binds (via the alpha chain) {\sf GA-rich\ promoters}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain ets RII regulatory region homology #labcl
#domain ets DNA-binding domain homology #label ETS
#length 454 #molecular-weight 51363 #checksum 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA binding; nucleus; transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Mus musculus #common_name house mouse
28-Feb-1992 #sequence_revision 23-May-1997 #text_ci
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#type complete
protein alpha (
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Pred. No. 6.37e-106;
61; Mismatches 61;
     chain -
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Gaps 15;

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##cross-references GDB:138476; OMIM:600609
#P_Position 21921-71922.1
GA-binding protein is a heterotetramer of
                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type protein
##residues 237-248;429-448 ##label VIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA; protein
##residues 1-454 ##label WAT
    180
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                                                                                                                                                                                             Local
                                                                                    NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDF-QRL 179
                                                                                                                           EQERLGIPYDPIQWSTDQVLHWVVWVMKEFSMTDIDLTTL-NISGRELCSLNQEDFFQRV 234
TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP
                                    -PR--GEILWSHLELLR-K---YVLASQE--QQMNE-IVTI-DQP-VQIIPAS-VQSATP 281
                                                                                                                                                                      ch 19.8%;
1 Similarity 41.6%;
101; Conservative
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Virbasius, J.V.; Virbasius, C.A.; Scarpulla, R.C.

Genes Dev. (1993) 7:380-392

Identity of GABP with NRF-2, a multisubunit activator of cytochrome oxidase expression, reveals a cellular role an ETS domain activator of viral promoters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardot, P.; Pastler, D.; Lacorte, J.M.; Mangeney, M.; Zannis V.I.; Chambaz, J.
Blochemistry (1994) 33:12139-12148
Purification and characterization of nuclear factors binding to the negative regulatory element D of human apolipoprotein A-II promoter: a negative regulatory effect is reversed by GABP, an ets-related protein.
                                                                                                                                                                                                                                                          #domain ets RII regulatory region homology #label
#domain ets DNA-binding domain homology #label ET9
#length 454 #molecular-weight 51311 #checksum 3079
                                                                                                                                                                                                                                                                                                                                                                 adenovirus E4 genes
#superfamily transcription factor elg; ets DNA-binding
homology; ets RII regulatory region homology
                                                                                                                                                                                                                                                                                                                                                                                                                                   known to promote transcription of apolipoprotein A-II, cytochrom c oxidase chain IV, ATPase beta chain, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor that binds (via the alpha chain) \mathsf{GA}\text{-rich} promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-type chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Handa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
26-34,'A',36,'X',38,'X',40-46;151-165;167-174;350-359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Biol. (1993) 13:1385-1391 cloning of transcription factor E4TF1 subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence extracted from NCBI backbone (NCBIP:125762) parts of this sequence were determined by protein
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                                                                                                                                                                      Score 649; DB 1; Lo
Pred. No. 4.38e-105;
60; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                   transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K.; Yamaguchi,
                                                                                                                                                                                                               Length 454;
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174-245
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#journal Mol. Cell. Biol. (1995) 15:102-111
#title Four structurally distinct, non-DNA-binding subunits
nuclear respiratory factor 2 share a conserved
transcriptional activation domain.
#cross-references_MUID:95097980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 EQERLGIPYDPIQWSTDQVLHWVVWVMKEFSMTDIDLTTL-NISGRELCSLNQEDFFQRV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references EMBL:U13044; NID:g531892; PID:g531893
IFICATION #superfamily transcription factor elg; ets DNA-binding homology; ets RII regulatory region homology
                                                                                                                                                                                                     360
                                                                                                                                                                                                                                     397
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                                                                                                                                                                                                                                                                                                                                     TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNS 299
                                                                                                                                                                                                                                                                                                                                                        TTIKVINRCAKA-AKVQ-RAPRISGEDRSSP-GNRTGN--NGQIQLWQFLLELLTDKDAR 336
                                                                                                                                                                                                                                                                                                                                                                                                       TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDF-QRL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKF
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                                                                                                                                                                                                                                                                  NCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                         -PR--GEILWSHLELLR-K---YVLASQE--QQMNE-IVTI-DQP-VQIIPAS-VQSATP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNS
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Similarity 40.7%;
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S28823
S28819
                                               transforming protein ets-6
#formal_name Drosophila melanogaster
31_Dec-1993 #sequence_revision 31-Dec-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear respiratory factor-2 subunit alpha #formal_name Homo sapiens #common_name man 29-May-1998 #sequence_revision 29-May-1998
                                                                                                transcription factor ets-21C melanogaster) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain ets RII regulatory region homology #length 454 #molecular-weight 51408 #checksum
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                                                                                                                               #type fragment
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Pred. No. 3.35e-103;
61; Mismatches 63;
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FEATURE
95-173
SUMMARY
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FEATURE
8-86
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##Cross-references FlyBase:FBgn0004510
CLASSIFICATION #superfamily ets DNA-binding domain homology
KEYWORDS DNA binding
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Best Local Similarity 80.4%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
#journal
#title
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                 137 KNKPAMNYEKLSRALRYYYDGDMISKVSGKRFAYKFD 173
 327
                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##residues 1-211 ##label PRI
##cross-references EMBL:X58481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 LGPTS-SRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGER 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references FlyBase:FBgn0005660 htrons 64/2
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##residues 1-103 ##label CHE
##cross-references EMBL:M88475
                                                                                                                                      y Match 15.0%;
Local Similarity 59.8%;
hes 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               ##status
                                                                                 15
KSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFD 363
                                                                                                                                                                                                                                                                                                                                                                                                             Pribyl, L.J.; Watson, D.K.; Schulz, R.A.; Papas, T.S. Oncogene (1991) 6:1175-1183
D-clg, a member of the Drosophila ets gene family: sequence, expression and evolutionary comparison.

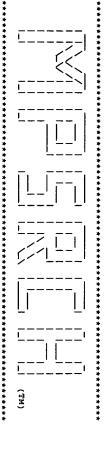
S24300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily transcription factor erg; ets DNA-binding domain
homology; ets RII regulatory region homology
DNA binding; nucleus; transcription factor
                                                                                                                                                                                                     #domain ets DNA-binding domain homology #label #length 211 #molecular-weight 23603 #checksum 604/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Drosophila melanogaster
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S. Dev. Biol. (1992) 151:176-191
Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain ets DNA-binding domain homology #label #length 103 #checksum 5825
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                                                                                                                                   Score 493; DB 2; Length 211; Pred. No. 8.80e-73; 24; Mismatches 14; Indels
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Pred. No. 1.19e-99;
13; Mismatches 6;
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Search completed: Wed Apr

7

09:33:14 1999

Job time : 68 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

aun on: Wed Apr 7 09:33:30 1999; MasPar time 13.48 Seconds 898.017 Million cell updates/seconds

Title: >US-08-878-177-2
Description: (1-451) from US08878177.pep
Perfect Score: 3286

Perfect Score: 3286
Sequence: 1 MASTIKEALSVVSEDQSLFE.....IYPNTRLPAAHMPSHLGTYY 451

Scoring table: PAM 150 Gap 11

earched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 49.266; Variance 82.055; scale 0.600

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UMMARIES

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
|------------|-----------------------|------------|------------|------------------------|-----------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------|------------------------|
| 372 | 418 | 418 | 420 | 422 | 429 | 431 | 437 | 443 | 443 | 444 | 443 | 454 | 456 | 460 | 460 | 459 | 469 | 469 | 474 | 480 | 482 |
| 11.3 | 12.7 | 12.7 | 12.8 | 12.8 | | 13.1 | 13.3 | 13.5 | | 13.5 | | 13.8 | 13.9 | | | 14.0 | | 14.3 | | 14.6 | 14.7 |
| 619 | 431 | 405 | 409 | 407 | 430 | 429 | 428 | 555 | 551 | 341 | 335 | 510 | 250 | 477 | 477 | 64 | 551 | 548 | 110 | 479 | 669 |
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| ELF1_HUMAN | SAPA HUMAN | SAPB_HUMAN | ELK3_MOUSE | ELK3_HUMAN | SAPA_MOUSE | ELK1_MOUSE | ELK1_HUMAN | ETV4_MOUSE | ETV4_HUMAN | ETV2_HUMAN | ETV2_MOUSE | ERM_HUMAN | ETV3_HUMAN | ETV1_HUMAN | ETV1_MOUSE | ETS3_DROME | ERF_MOUSE | ERF_HUMAN | ETS2_LYTVA | ETS2_CHICK | MYBE_AVILE |
| ELATED TRA | SERUM RESPONSE FACTOR | | _ | ETS-DOMAIN PROTEIN ELK | SERUM RESPONSE FACTOR | ETS-DOMAIN PROTEIN ELK | ETS-DOMAIN PROTEIN ELK | POLYOMAVIRUS ENHANCER | ADENOVIRUS E1A ENHANCE | ETS-RELATED PROTEIN 71 | ETS-RELATED PROTEIN 71 | ETS-RELATED PROTEIN ER | ETS-RELATED PROTEIN PE | ETS TRANSLOCATION VARI | ER81 PROTEIN (ETS TRAN | DNA-BINDING PROTEIN D- | ETS-DOMAIN TRANSCRIPTI | ETS-DOMAIN TRANSCRIPTI | C-ETS-2 PROTEIN (FRAGM | C-ETS-2 PROTEIN. | P135-GAG-MYB-ETS TRANS |
| 5.39e-56 | 1.50e-66 | 1.50e-66 | 5.18e-67 | 1.78e-67 | 4.26e-69 | 1.46e-69 | 5.91e-71 | 2.38e-72 | 2.38e-72 | 1.39e-72 | 2.38e-72 | 6.47e-75 | 2.21e-75 | 2.56e-76 | 2.56e-76 | 4.39e-76 | 2.00e-78 | 2.00e-78 | 1.34e-79 | 5.24e-81 | 1.78e-81 |

ALIGNMENTS

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PRC_HUMAN STANDARD; PRT; 462 AA.

11308;
01-UUL-1989 (REL. 11, CREATED)
01-UUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-UUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-UUL-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-CUT-1986 (REL. 13, LAST SHOUNCE UPDATE)
01-CUT-1986 (REL. 14, LAST SEQUENCE UPDATE)
01-CUT-1986 (REL. 12, LAST SEQUENCE UPD
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Best Local S
Matches 40
                                                                                                 SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 92396239.
DELATTRE O., ZUCMAN J., PLC
PETER M., KOVAR H., JOUBERT
NATURE 359:162-165(1992).
                                                    SEQUENCE FROM N.A.
MEDLINE; 93075640.
WATSON D.K., SMYTH F
PAPAS T.S., SETH A.;
CELL GROWTH DIFFER.
                                                                                                                                                                                        01-JUL-1993 (REL.
01-JUL-1993 (REL.
01-NOV-1997 (REL.
FLI-1 ONCOGENE (ER
                                                                                                                                                                                                                        FLI1_HUMAN
Q01543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
CHAIN
DNA_BIND
SEQUENCE
              SEQUENCE FROM N.A.
MEDLINE: 93007976.
PRASAD D.D., RAO V.N., REDDY E
CANCER RES. 52:5833-5837(1992)
SEQUENCE
                                                                                                                                                          EUTHERIA;
                                                                                                                                                                                                                                                                418
                                                                                                                                                                                                                                                                               429
                                                                                                                                                                                                                                                                                              358
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                                                                                                                                                                 SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAYKEDEHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNEVAPHPPALPYTSSSF
                                                                                                                                                                                                                                                                                                                                                                                        YAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSF
                                                                                                                                                                                                                                                                                                                                    NSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                                                                                                                                                                                                                          PT-QSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSS
                                                                                                                                                                                                                                                                                                                                                                   PTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSS
                                                                                                                                                                                                                                                                                                                           NSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
FROM
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100
294
462
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larity 89.4%;
Conservative
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,L. 26, I
£L. 35,
3 (ERGB
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                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462
462
374
52031
                                                                   F.E.,
                                                                                                          JOUBERT
                                                    3:705-713(1992).
                                                                                                                                                                                       , CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR).
                                                                                                          PLOUGASTEL
BERT I., DE
                                                                    THOMPSON D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2991; DB 1;
Pred. No. 0.00e+00;
26; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFORMING PROTEIN I
TRANSFORMING PROTEIN I
ETS-DOMAIN.
FCCCC2D2B CRC32;
                     m
                                                                                                                                                                 VERTEBRATA;
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                                                                                                          B., I
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                                                                                                          DESMAZE C., 1
3 P., ROULEAU
                                                                                                                                                                                                                                                                              462
                                                                    CHENG
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                                                                                                                                                                  TETRAPODA;
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                                                                   J.Q.,
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                                                                                                          MELOT
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                                                                    TESTA
                                                                                                                                                                  MAMMALIA;
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                                                                                                                                                                                                                                                                                                            428
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Best Local S
Matches 30
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EMBL; X67001; G32530; - .

EMBL; M89833; G182189; - .

EMBL; S45205; G257354; - .

EMBL; M93255; G182660; - .

PDB; 1FL1; 15-SEP-95.

TRANSFAC; T02066; - .
                                                                                                                                                                                                                                                                                                                                                                                  PROTO-ONCOGENE; ODNA_BIND 281
CONFLICT 69
CONFLICT 77
CONFLICT 130
CONFLICT 323
CONFLICT 323
CONFLICT 323
CONFLICT 426
SEQUENCE 452 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
MEDLINE; 93176799.
HROMAS R., MAY W., D:
BECK E., KLEMSZ M.J.
BIOCHIM. BIOPHYS. AC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00345;
PROSITE; PS00346;
PROSITE; PS50061;
TRANSCRIPTION REGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95292091.

LIANG H., MAO X., OLEJNICZAK E.T., NETTESHEIM D.G., YU L MEADOWS R.P., THOMPSON C.B., FESIK S.W.;

MAT. STRUCT. BIOL. 1:871-875(1994).

-!- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATO
-!- SUBCILLULAR LOCATION: NUCLEAR.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- DISEASE: A FORM OF EWING'S SARCOMA IS CHARACTERIZED CHROMOSOMAL TRANSLOCATION T(11;22)(Q24;Q12) WHICH IN
                      358
416
                                           356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                 NASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                       SGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSA 295
                                                                                                                                                                                                              TINERRVIVPADPILWTQEHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLR
                                                                                                                                                                                                                                                           P-VRVNVKREYD--HMNGSRESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNM 117
FGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGSYY
                                                                NSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                      PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM 118
                                                                                                           PTQSKATQPSSS-TVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSS
                                                                                                                                                                                                    TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY NMR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345; ETS_DOMAIN_1; 1.
346; ETS_DOMAIN_2; 1.
061; ETS_DOMAIN_3; 1.
REGULATION; ACTIVATOR;
                                                                                                                                                                                                                                                                                                                                                                                    AA;
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77
130
133
323
391
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                                                                                                                                                                                                                                                                                                                                                                                ETS-DOMAIN.
E -> V (IN REF. 4).
MISSING (IN REF. 4).
P -> A (IN REF. 4).
P -> V (IN REF. 4).
C -> Q (IN REF. 3).
C -> Q (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2 AND 4).
MISSING (IN REF. 2 AND 4).
                                                                                                                                                                                                                                                                                                                                       Score
Pred.
85; M
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                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                 2348;
No. 0.
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                                                                                                                                                                                                                                                                                                                                                 DB 1;
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RESULT
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Best Local
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P26323;

01-MAY-1992 (REL. 22, CR

01-MAY-1992 (REL. 22, LA

01-NOV-1995 (REL. 32, LA

RETROVIRAL INTEGRATION S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE: 93275657.
ZHANG L., LEMARCHA
BERNSTEIN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. F
THE DNA SEQUENCE 5'C[CA]GGAAGT-3'.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: EXPRESSED IN BOTH HEMATOPOIETIC AND
NONHEMATOPOIETIC TISSUES.
-!- INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLONES
F-MULY INSERTIONS UP-STREAM OF THE FLI-1 LOCUS.
-!- DISSASE: INVOLVED IN ERYTHROLEUKEMIA INDUCTION BY FRIEND
LEUKEMIA VIRUS (F-MULV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEN-DAVID Y., GIDDENS E.B.,
GENES DEV. 5:908-918(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE EMBL; X59421; G50975; - EMBL; X59421; G50975; - PIR; S17403, S17403.
TRANSFAC; T01408; - T01408; MGI: 95554; FLI1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BALB/C; TIS MEDLINE; 91257578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLI1 OR FLI-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTO-ONCOGENE.
DNA_BIND 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
TRANSCRIPTION REGULATION; ACTIVATO
                                                                                           179
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                                                                                                                                                                                  119
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    239
                                            236
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                                                                                                                                                                                                                                                                                                                                                                                        MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQPHKINPLPPQQEWINQ 60
TINERRVIVPADPILWIQEHVRQWLEWAIKEYGLMEIDISFFQNMDGKELCKMNKEDFLR 177
                                                                                                                                                                                                                                                                                               P-VRVNVKREYD--HMNGSRESPVDCSVSKCNKLVGGGEANPMNYNSYMDEKNGPPPPNM 117
                                                                                                                                                                                TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR
                                                                                                                                                                                                                                                                       PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM
                                                                                                                                                                                                                                                                                                                                                                 MASTIKEALSVVSEDQSLFECAYGSP-HLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
305; Conser
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larity 66.7%;
Conservative
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22, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
37, CTTE PROTEIN FLI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 E
51002 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2339;
Pred. No. 0.
85; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local S
Matches 30
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01-FEB-1995
01-FEB-1995
01-FEB-1995
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SEQUENCE
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PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
TRANSCRIPTION REGULATION; ACTIVATOR;
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MECH. DEV. 44:109-121(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEYER D., WOLFF C.M.,
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DEVELOPMENTAL STAGE: EXPRESSED
SIMILARITY: BELONGS TO THE ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGAASQYWTSPTAGIYPNPSVPRHPNTHVPSHLGSYY 452
|:|:: || |||:|||| : | | :|:||||:||
FAAPNPYWNSPTGGIYPN-T--RLPAAHMPSHLGTYY 451
RYAYKFDEHGIAQALQPHPTDTSMYKYPSEFSYMPSYHSHQQKVNFVPSHPSSMPVTSSG 415
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                                                                                    TINERRVIVPADPALWSQDHVRQWLEWAIKEYGLVEIDCSLFQNIDGKELCKMSKEDFLR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                             P-MRVNIKREYE--HMNGSRESPVDCSINKCSKLIGGSEGNAMTY-TYMDEKNGPPPPNM 116
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                                                                                                                                                                                           SPVTKSPPMGGTQNVNKSGDQQRSQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                       PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM
                                                                                                                                                                    HPTQSKATQPSSSTVPKT-EDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDS
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| Similarity 65.9%;
| 302; Conservative
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453 AA;
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51015 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 0.00e+00
85; Mismatches 5
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Best Local S
Matches 20
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Q01414;
01-FEB-1995
01-FEB-1995
01-FEB-1995
ERG_PROTEIN
ERG.
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PROSITE;
PROSITE;
PROSITE;
SEQUENCE FROM N.A.

MEDLINE; 93091246.

QI S., CHEN Z.Q., PAPAS T.S., LAUT

QI S., SI:127-129(1992).

-I- SUBCELLULAR LOCATION: NUCLEAR.

-I- SIMILARITY: BELONGS TO THE ETS
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERG_MOUSE P81270;
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-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELLONGS TO THE ETS FAMILY.
EMBL, S66169; G436277; -.
                                                                                                                                                                 EUECHINOIDEA.
                                                                                                                                                                                    LYTECHINUS VARIEGATUS (SEA URCHIN) EUKARYOTA; METAZOA; ECHINODERMATA;
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NON_TER
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15-JUL-1998 (REL. 36, LAST SEQUENCE UF
15-JUL-1998 (REL. 36, LAST ANNOTATION
TRANSFORMING PROTEIN ERG (FRAGMENT).
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|SMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPE
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; PS00346; ETS_DOMAIN_2; 1.
; PS50061; ETS_DOMAIN_3; 1.
pROTEIN; TRANSFORMING PROTEIN; DNA-BINDING;
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                                                                                                                                                                                                                                                                      (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
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llarity 94.5%;
Conservative
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Pred. No. 0.00e+00;
9; Mismatches 2
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                                                                         LAUTENBERGER
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         ETS FAMILY
                                                                                                                                                                                    ECHINOZOA;
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                                                                                                                                                                                    ECHINOIDEA;
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  Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                  DEV. BIOL. 151:176-191(1992).
-!- SUBCELLULAR LOCATION: NUCLEAL
-!- SINGLEARINY: BELONGS TO THE EX-
EMBL; X68259; G7943; -.
EMBL; X58481; G7941; ALT_INIT.
EMBL; X58481; G552088; -.
PIR; S24300; S24300.
PIR; S28822; S28822.
PIR; S37616; S37616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M81067; G161311; -.

PROSITE; PS00345; ETS_DOMAIN_2; 1.

PROSITE; PS00346; ETS_DOMAIN_3; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

NUCLEAR PROTEIN; DNA-BINDING.

NON_TER 1 1

DNA_BIND <1 84

SEQUENCE 173 AA; 19690 MW; 603
                                                                                                                                                                                          FLYBASE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q04688;
Q04688;
Q1-JUN-1994 (REL. 29, CREATED)
Q1-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
Q1-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DNA-BINDING PROTEIN D-ELG.
ETS97D OR ELG.
                                                                                                                                                 PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 93096481.
THE S.M., XIE X., SMYTH F.,
ONCOGENE 7:2471-2478(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 298-449 FROM N.A. MEDLINE; 92249640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIBYL L.J., WATSON D.K., SO
ONCOGENE 6:1175-1183(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF MEDLINE; 913
                                                                                                       DNA-BINDING;
                                                                                                                                                                                                                                     TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROSOPHILA MELANOGASTER (FRUIT |
EUKARYOTA; METAZOA; ARTHROPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELG_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNEVAPHPPALPVTSSSFFAAPNPYWNSPTGG-IYPNTRL--P-AAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNFVGT-PIN-PSTNASLFSSHSSYWSSPTGANIYPSGHVTHPHASHMSSHIGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129;
                                                                                                                    ; FBgn0004510; Ets97D.; PS0345; ETS_DOMAIN_1; 1; PS00345; ETS_DOMAIN_2; 1; PS50061; ETS_DOMAIN_3; 1; PS50061; ETS_DOMAIN_3; 1
  Similarity 39.6% 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 29.2%;
Similarity 73.3%;
129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      BUNTING M., KARIM F
L. 151:176-191(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91319397
                                                                                  346
464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323-463 FROM
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                     20.1%;
                                                                                    52658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            KARIM F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHULZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 959; DB 1; I
Pred. No. 2.43e-197;
27; Mismatches 12;
Score 660; DB 1; Le
Pred. No. 5.29e-124;
62; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPAS
                                                                                                       ETS-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETS-DOMAIN
6039FEE1
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                                                                                  A7589B7A CRC32;
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                                      Length 464;
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  Indels
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  12;
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Gaps
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S
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CSIENCE 279:1037-1041(1998).

-!- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERPRETATS (GA REPEATS).

-!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.

-!- SIMILARITY: BELONGS TO THE ETS FAMILY.

EMBL: M74515; G193383; -.

EMBL: M74515; G193383; -.

TRANSFAC: T00298: -.

TRANSFAC: T01402: -.

MGD: MGT. MGT. CATA.
                                                                                                   Query Match
Best Local
                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                        MEDLINE; YELLOW A.H., F BATCHELOR A.H., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ULT 8
GABA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                           LAMARCO K., THOMPSON C.C.,
SCIENCE 253:789-792(1991).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000422;
01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GA BINDING PROTEIN ALPHA CHAIN (GABP-ALPHA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                           PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 91343912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GABPA.
                                                                                                                                                                                                           MGD; MGI:95610;
                      235
                                             121
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                  -PR--GEILWSHLELLR-K---YVLASQE--QQMNE-IVTI-DQP-VQIIPAS-VPPATP 281
                                                        AYKFD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP
TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PRDPGNIFWTHLQLLKE--CNFV-SVVHKRAEE-ORKPKOPRIMSANSISTN-SGGSLS
                                                                                         1 Similarity
101; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426
                                                                                                                                      454 AA;
                                                                                                                                                  320
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                           GABPA.
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                                                                                                     19.98;
                                                                                                                                      51363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               .c.
                                                                                                                                                                                                                                                                                                                                                                                                                                  BYERS
                                                                                       Score 653; DB 1; Lu
Pred. No. 2.61e-122;
61; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                      ETS-DOMAIN.
; C3B45F76 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                OWI
                                                                                                                                                                                                                                                                                                                                                                                                                                E.M.,
                                                                                                                                                                                                                                                                                                                                       INTERACTING WITH
                                                                                                                Length
                                                                                                                                                             PROTEIN;
                                                                                                                                                                                                                                                                                                                BETA SUBUNITS
                                                                                         Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MCKNIGHT
                                                                                                                                                               3D-STRUCTURE
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Best Local
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GABA_HUMAN STANDARD; PRT; 454 AA.

(06546; (01293);
(01-FEB-1995 (REL. 31, CREATED)
(11-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

GA BINDING PROTEIN ALPHA CHAIN (GABP-ALPHA SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-60) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT ALPHA).

E4TF1A OR GABPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUGNEJA S., VIRBASIUS J.V., SCARPULLA R.C.;
MOL. CELL. BIOL. 15:102-111(1995).
-i- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INT
RICH REPEATS (GA REPEATS). NECESSARY FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00345; ETS_DOMAIN_1; PROSITE: PS00346; ETS_DOMAIN_2; PROSITE: PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 9318 WATANABE H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T01390; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 95097980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 600609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                              ADENOVIRUS E4 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKF
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TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNS
                                                                                                                                                           TPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP
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                                                                                                               TTIKVIN-SSAKAAKVQ-RAPRISGEDRSSP-GNRTGN--NGQIQLWQFLLELLTDKDAR
                                                                                                                                                                                    NCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D13318; G286027; -. U13044; G531893; -.
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289
440
454 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-BINDING; NUCLEAR PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                              ETS-DOMAIN.
SS -> RC (IN REF. 2)
A -> V (IN REF. 2).
W; E0EA85D4 CRC32;
                                                                                                                                                                                                                                                                                                                                      Score 649; DB 1; L
Pred. No. 2.42e-121;
60; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.-I.,
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CHEN T., BUNTING M., KARIM F.D.
DEV. BTOL. 151:176-191(1992).
-!- SUBCELLULAR LOCATION: NUCL
-!- SUBLARITY: BELONGS TO THE
EMBL; M848475; G157198; -.
PIR; S28823; S28823
SEQUENCE FROM N.A.

TISSUE-OVARY;

SALVATI A.L.; MORABITO S., MERENDINO X., C
SUBMITTED (APR.1992) TO EMBL/GENBANK/DDBJ
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                 WEDLINE; 90384849.
STIEGLER P., WOLFF C.M., BALTZINGER M., HII
MEYER D. GHYSDAEL J., STEHELIN D., BEFORT
NUCLEIC ACIDS RES. 18:5298-5298(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (REL.
01-NOV-1990 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLYBASE; FBgn0005660; Ets21C.
PROSITE; PS00346; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDI
01-FEB-1995 (REL. 31, LAST ANNOTATION UI
DNA-BINDING PROTEIN D-ETS-6 (FRAGMENT).
ETS21C OR ETS-6.
DROSOPHILA MELANOGASTER (FRUIT FLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETS6_DROME P29776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XENOPUS LAEVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETS-1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                         METAZOA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFRICAN CLAWED AZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16, CREATED)
16, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDAT
(XE1-B) (FRAGMENT).
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Pred. No. 4.54e-
13; Mismatches
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No. 4.54e-115;
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ORT N., R
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P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQ FTT
                                                Query Match
Best Local Similarity
Matches 62; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (REL. 1
01-NOV-1990 (REL. 1
01-NOV-1997 (REL. 3
C-ETS-1A PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P18755;
01-NOV-1990
01-NOV-1990
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S11224;
TRANSFAC; T02
PROSITE; PS00
PROSITE; PS00
PROSITE; PS50
                                                                                                                         SIMILAR
SEQUENCE
                                                                                                                                                                                                                                        VARSPLIC DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIEGLER P., WOLFF C.M., BALTZINGER M., HIRZLIN MEYER D., GHYSDAEL J., STEHELLN D., BEFORT N., FUNCLEIC ACIDS RES. 18:5298-5298 (1990).

- I SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52692; G64615; PIR; S11225; S11225.
                                                                                                                                                                                                                                                                                                                                                                                                        FIRST 203 AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XENOPUS LAEVIS (AFR EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-BINDING; NUCLEAR PROTEIN; PHOSPHORYLATION.
NON_TER 1 1
DNA_BIND 162 242 ETS-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52691; G64617;
EMBL; X65166; G517230;
PIR; S11224; S11224.
                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                             PROSITE; PS5
                                                                                                                                                                                                                                                                                                                                                       TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ET1A_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
             307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137
DRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                           PS00345; ETS_DOMAIN_1;
PS00346; ETS_DOMAIN_2;
PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00345; ETS_DOMAIN_1;
PS00346; ETS_DOMAIN_2;
PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90384849.
                                                                                                                         438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
                                                                                                                                                                                                       061; E1.
NUCLEAR P.
1 203
1 412
153
                                            15.0%;
larity 59.0%;
Conservative
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larity 59.0%;
Conservative
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109
                                                                                                                                                                                 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AFRICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16,
35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
109
                                                                                                                         438
50267
                                                                                                                                                                               279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30772
                                                                                                                                                                                                                                                                             PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST
LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLAWED FROG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                           MW;
                                                                                                                     IN; ALTERNATIVE SPLICING; PHOSPHORYLATION.
MISSING (IN C-ETS-1A').
ETS-DOMAIN.
PHOSPHORYLATION (BY CAM-KINASE)
(POTENTIAL).
PHOSPHORYLATION (BY CAM-KINASE)
PHOSPHORYLATION (BY CAM-KINASE)
(POTENTIAL).
98.9% IDENTITY TO C-ETS-1B PROTEIN.
98.9% IDENTITY TO C-ETS-1B PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                          THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                              Score 492; DB 1;
Pred. No. 7.87e-84;
20; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 492; DB 1;
Pred. No. 7.87e-84;
20; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETS-DOMAIN.
PHOSPHORYLATION (BY CAM-KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
6EF0772C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                               RISE
                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               TO C-ETS-1A'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N J.,
                                                                                Length 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LACKING
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENAN
P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMPHIBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268;
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                                                Gaps
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RESULT
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P27577; 061403;
01-AUG-1992 (REL. 23, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUE
15-JUL-1998 (REL. 36, LAST ANNOT
C-ETS-1 PROTEIN (P54).
ETS1 OR ETS-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA: PROTENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: NUCLEAL
-!- SIMILARITY: BELONGS TO THE E-
EMBL; M58482; G193192; -.
EMBL; X53953; G50871; -.
EMBL; X55787; G296023; -.
PIR; A30487; A30487.
                                                    CONFLICT
CON
  CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MG1:9343; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS0061; ETS_DOMAIN_3; 1.

PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1ETC; 29-JAN-96.
PDB; 1ETD; 29-JAN-96.
TRANSFAC; T00111; -.
MGD; MGI:95455; ETS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C: TISSUE-THYMUS;
MEDLINE: 90299137.
GUNTHER C.V., NYE J.A., BRYNER
GENES DEV. 4:667-679(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WATSON D.K., SETH A., SMYTH F
(IN) ONCOCENESIS, PAPAS T.S.,
COMPANY, HOUSTON, (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTO-ONCOGENE; I PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DONALDSON L.W., PETERSEN
EMBO J. 15:125-134(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96176767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 332-415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONCOGENE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEN J.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90370376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKF
413
440
                                                       5:277-285(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PETERSEN J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-STRUCTURE
                                                          ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR
                   ETS-DOMAIN.

D -> E (IN REF. 3).

L -> S (IN REF. 3).

AT -> SY (IN REF. 3).

G -> P (IN REF. 3).

E -> D (IN REF. 3).

D -> V (IN REF. 3).

D -> V (IN REF. 3).

D -> V (IN REF. 3).

D -> C (IN REF. 3).

D -> C (IN REF. 3).

D -> C (IN REF. 3).

A -> C (IN REF. 3).

A -> N (IN REF. 3).

A -> N (IN REF. 3).

C -> N (IN REF. 3).

A -> N (IN REF. 3).

C -> N (IN REF. 3).
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ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRAVES B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWEINFEST C, PP. 221-232,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRAVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440
                                      N REF. 3).
N REF. 3).
        REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCINTOSH L.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GULF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLICING
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RESULT RESULT RESULT REPORT RE
Query Match
Best Local Similarity
""" 62; Conserv
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 89083
REDDY E.S.P.,
ONCOGENE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990
01-APR-1990
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                    -I- ALTERNATIVE PRODUCTS: ISOFORMS OF ETS-1
ALTERNATIVE SPLICING.
-I- SIMILARITY: BELDORGS TO THE ETS FAMILY.
EMBL; X14798; G29882; -.
EMBL; X14798; G296642; -.
EMBL; J04101; G182269; -.
EMBL; J04066; TVHUET.
PIR; A32066; TVHUET.
PIR; S10086; S10086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WERNER M.H., CLORE G.M., FISHER C.L., FISHER R.J., TRINH L., SHILDACH J., GRONENBORN A.M.;
CELL 83:761-771(1995).

-i- SUBCELLULAR LOCATION: NUCLEAR.

-i- PTM: ISOFORMS OF ETS-1 ARE ALSO GENERATED BY DIFFERENTIAL PHOSPHORYLATION.

-i- DISEASE: ETS IS RESPONSIBLE FOR ERYTHROBLAST AND FIBROBLAST TRANSFORMATION. THE JUXIAPOSITION OF THE INTERFERON AND C-ET PROTO-ONCOGENE MAY BE INVOLVED IN THE PATHOGENESIS OF HUMAN
                                                                                                                               DNA_BIND
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETS1
                                                                                                                                                                                  PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING;
                                                                                                                                                                                                                                                                                                      PDB; 2STT; 12-MAR-97
PDB; 2STW; 12-MAR-97
TRANSFAC; T00112; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 89042086. WATSON D.K., MCWII SCHWEINFEST C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-ETS-1 PROTEIN (P54)
                                                                                                                                                  PHOSPHORYLATION;
DNA_BIND 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 320-415. MEDLINE; 96097120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE: 89083219.
REDDY E.S. P., RAO V.N.;
ONCOGENE RES. 3:239-246(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P14921;
                                                                                                                                                                                                                                                                                      MIM; 164720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROC. NATL. ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONOCYTIC LEUKEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                         244
441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REL. 14,
(REL. 14,
(REL. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCWILLIAMS M.J.,
C.W., PAPAS T.S.;
ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%;
larity 59.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                      3D-STRUCTURE.
                                                                                                      415
330
50408
                                         14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)

LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

(C-ETS-1A AND C-ETS-1B)
                                                                                                         , WM
               Score 490; DB 1;
Pred. No. 2.33e-83;
20; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 490; DB 1;
Pred. No. 2.33e-83;
20; Mismatches 23
                                                                                                      ETS-DOMAIN.
MISSING (IN C-ETS-1B)
; 958AFA4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85:7862-7866(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAPIS P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAUTENBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAN
                                                             Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BΕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Conservative

Indels

0

Gaps

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RESULT
ID E1
AC P4
AC P7
DT 01
DT 01
DE C-
GN E1
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RA MEDLINE: 94187072.

RA BELLACOSA A., DATTA K., BEAR S.E., PATRIOTIS C., LAZO P.A.,

COPELAND N.G., JENKINS N.A., TSICHLIS P.N.;

RA COPELAND N.G., JENKINS N.A., TSICHLIS P.N.;

C. -!- SUBCELLULAR LOCATION: NUCLEAR.

C. -!- SUBCELLULAR LOCATION: NUCLEAR.

C. -!- SUBLELLULAR LOCATION: NUCLEAR.

C. -!- SUBLELLULAR LOCATION: THE ETS FAMILY.

C. -!- SUBLELLULAR LOCATION: THE ETS FAMILY.

C. -!- SUBLELLULAR LOCATION: NUCLEAR.

C. -!- SUBLELLULAR LOCATION: NUCLEAR PROTEIN; ALTERNATIVE SPLICING;

PROSITE: PS00345; ETS_DOMAIN_3; 1.

DR PROSITE: PS00346; ETS_DOMAIN_3; 1.

PROTO-ONCOGENE; DNA-BINDING; NUCLEAR PROTEIN; ALTERNATIVE SPLICING;

PROSITE: PS00345; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.9%;
Best Local Similarity 59.0%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA1156;
PA1156;
PA1156;
PA1156;
O1-FEB-1995 (REL. 31, CREATED)
O1-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
C-ETS-1 PROTEIN (PS4).
FS1 OR ETS-1.
RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION.
DNA_BIND 335 4
SEQUENCE 441 AA;
                                                                                            415 E'
50423 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
7 09:34:17 1999
                                                                                                                                                                                                                                                                                                                                                                                 Score 490; DB 1; Lo
Pred. No. 2.33e-83;
20; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETS-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1C04335A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 441;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
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Search completed: Wed Apr Job time : 47 secs.